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If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: Q9QZM7; 733 AA
Date run: 2007-11-13 20:35:31 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.16 [Mar-25-2007]
Database: UniProtKB Homo sapiens
82,088 sequences; 35,064,127 total letters
UniProt Knowledgebase Release 12.4 consists of:
UniProtKB/Swiss-Prot Release 54.4 of 23-Oct-2007: 287050 entries
UniProtKB/TrEMBL Release 37.4 of 23-Oct-2007: 4988379 entries

List of potentially matching sequences

Send selected sequences to

Include query sequence

Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr Q5BJG2	_HUMAN Fibroblast growth factor receptor 1 (Fms-related...	1420	0.0
<input type="checkbox"/>	sp_vs P11362-14	Isoform 15 of P11362 - Homo sapiens (Human) [FGF...	1420	0.0
<input type="checkbox"/>	sp_vs P11362-3	Isoform 6 of P11362 - Homo sapiens (Human) [FGFR1...	1415	0.0
<input type="checkbox"/>	sp_vs P11362-4	Isoform 8 of P11362 - Homo sapiens (Human) [FGFR1...	1407	0.0
<input type="checkbox"/>	sp_vs P11362-7	Isoform 14 of P11362 - Homo sapiens (Human) [FGFR...	1357	0.0
<input type="checkbox"/>	sp P11362	FGFR1_HUMAN Basic fibroblast growth factor receptor 1 ...	1352	0.0
<input type="checkbox"/>	tr Q53H63	_HUMAN Fibroblast growth factor receptor 1 isoform 2 va...	1351	0.0
<input type="checkbox"/>	tr Q59H40	_HUMAN Fibroblast growth factor receptor 1 isoform 1 va...	1344	0.0
<input type="checkbox"/>	sp_vs P11362-2	Isoform 4 of P11362 - Homo sapiens (Human) [FGFR1...	1344	0.0
<input type="checkbox"/>	sp_vs P11362-5	Isoform 10 of P11362 - Homo sapiens (Human) [FGFR...	1275	0.0
<input type="checkbox"/>	sp_vs P11362-6	Isoform 12 of P11362 - Homo sapiens (Human) [FGFR...	1266	0.0
<input type="checkbox"/>	sp_vs P21802-3	Isoform 3 of P21802 - Homo sapiens (Human) [FGFR2...	1108	0.0
<input type="checkbox"/>	sp_vs P21802-18	Isoform 18 of P21802 - Homo sapiens (Human) [FGF...	1100	0.0
<input type="checkbox"/>	sp P21802	FGFR2_HUMAN Fibroblast growth factor receptor 2 precu...	1065	0.0
<input type="checkbox"/>	sp_vs P21802-5	Isoform 5 of P21802 - Homo sapiens (Human) [FGFR2...	1057	0.0
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<input type="checkbox"/>	sp_vs P21802-17	Isoform 17 of P21802 - Homo sapiens (Human) [FGF...	1034	0.0
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<input type="checkbox"/>	tr Q1KHY5	_HUMAN Fibroblast growth factor receptor 2 (Bacteria-ex...	1011	0.0
<input type="checkbox"/>	sp_vs P21802-6	Isoform 6 of P21802 - Homo sapiens (Human) [FGFR2...	1011	0.0
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<input type="checkbox"/>	tr	Q8NI16	_HUMAN Fibroblast growth factor receptor 3 (Fragment) [...	929	0.0
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<input type="checkbox"/>	tr	Q8TDA0	_HUMAN Fibroblast growth factor receptor 4 (Fibroblast ...	839	0.0
<input type="checkbox"/>	tr	Q71TW8	_HUMAN Fibroblast growth factor receptor 4, soluble-for...	805	0.0
<input type="checkbox"/>	tr	Q8IXC7	_HUMAN Isoform of FGFR2 [FGFR2 AT-1] [Homo sapiens (Hum...	770	0.0
<input type="checkbox"/>	tr	Q96KE5	_HUMAN Fibroblast growth factor receptor 4 variant [Hom...	735	0.0
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<input type="checkbox"/>	tr	Q59FL9	_HUMAN Fibroblast growth factor receptor 3 isoform 1 va...	684	0.0
<input type="checkbox"/>	tr	A8E633	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	646	0.0
<input type="checkbox"/>	tr	Q0IJ44	_HUMAN FGFR3 protein (Fragment) [FGFR3] [Homo sapiens (...	646	0.0
<input type="checkbox"/>	sp_vs	P22607-3	Isoform 3 of P22607 - Homo sapiens (Human) [FGFR3...	625	e-178
<input type="checkbox"/>	tr	Q59F30	_HUMAN Fibroblast growth factor receptor 4 variant (Fra...	553	e-157
<input type="checkbox"/>	tr	Q9UD50	_HUMAN Fibroblast growth factor receptor subtype 1 (Fra...	516	e-146
<input type="checkbox"/>	sp_vs	P11362-18	Isoform 18 of P11362 - Homo sapiens (Human) [FGF...	468	e-131
<input type="checkbox"/>	tr	Q53G05	_HUMAN Fibroblast growth factor receptor 1 isoform 6 va...	467	e-131
<input type="checkbox"/>	sp_vs	P11362-16	Isoform 17 of P11362 - Homo sapiens (Human) [FGF...	463	e-130
<input type="checkbox"/>	sp_vs	P21802-19	Isoform 19 of P21802 - Homo sapiens (Human) [FGF...	375	e-103
<input type="checkbox"/>	sp	P35968	VGFR2_HUMAN Vascular endothelial growth factor recepto...	325	2e-88
<input type="checkbox"/>	tr	Q59EBO	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...	325	2e-88
<input type="checkbox"/>	tr	A2RRS0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	325	2e-88
<input type="checkbox"/>	tr	Q2VJ45	_HUMAN HOOK3-RET fusion protein [Homo sapiens (Human)]	323	5e-88
<input type="checkbox"/>	tr	Q9BTB0	_HUMAN Ret proto-oncogene [RET] [Homo sapiens (Human)]	323	6e-88
<input type="checkbox"/>	sp	P07949	RET_HUMAN Proto-oncogene tyrosine-protein kinase recep...	323	8e-88
<input type="checkbox"/>	sp	P17948	VGFR1_HUMAN Vascular endothelial growth factor recepto...	322	1e-87
<input type="checkbox"/>	tr	Q5TARI	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	322	1e-87
<input type="checkbox"/>	tr	Q9UMQ4	_HUMAN RET tyrosine kinase receptor (Fragment) [RET] [H...	319	1e-86
<input type="checkbox"/>	tr	Q15300	_HUMAN RET tyrosine kinase/cAMP protein kinase A subuni...	318	2e-86
<input type="checkbox"/>	tr	Q15850	_HUMAN Urf-ret protein [urf-ret] [Homo sapiens (Human)]	318	2e-86
<input type="checkbox"/>	sp	P35916	VGFR3_HUMAN Vascular endothelial growth factor recepto...	295	1e-79
<input type="checkbox"/>	tr	Q86W08	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	291	3e-78
<input type="checkbox"/>	tr	Q86W07	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	291	3e-78
<input type="checkbox"/>	tr	Q59GQ9	_HUMAN Fms-related tyrosine kinase 1 (Vascular endothel...	291	3e-78
<input type="checkbox"/>	tr	A3E342	_HUMAN IdVEGPR-1 (N2idVEGFR-1) [FLT1] [Homo sapiens (Hu...	290	8e-78
<input type="checkbox"/>	tr	Q86WV7	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	277	5e-74
<input type="checkbox"/>	sp	P07333	CSF1R_HUMAN Macrophage colony-stimulating factor 1 rec...	276	9e-74
<input type="checkbox"/>	tr	Q6IQ28	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	270	6e-72
<input type="checkbox"/>	sp	P10721	KIT_HUMAN Mast/stem cell growth factor receptor precu...	266	7e-71
<input type="checkbox"/>	tr	Q99662	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	266	7e-71
<input type="checkbox"/>	sp	P35590	TIE1_HUMAN Tyrosine-protein kinase receptor Tie-1 prec...	246	1e-64
<input type="checkbox"/>	tr	Q9HBS4	_HUMAN Putative uncharacterized protein [TIE1] [Homo sa...	246	1e-64
<input type="checkbox"/>	sp	Q02763	TIE2_HUMAN Angiopoietin-1 receptor precursor (EC 2.7.1...	240	7e-63
<input type="checkbox"/>	tr	Q5TCU2	_HUMAN TEK tyrosine kinase, endothelial (Venous malform...	240	7e-63
<input type="checkbox"/>	tr	Q59HG2	_HUMAN TEK tyrosine kinase variant (Fragment) [Homo sap...	240	7e-63
<input type="checkbox"/>	tr	Q8IV34	_HUMAN TEK tyrosine kinase, endothelial (Venous malform...	239	2e-62
<input type="checkbox"/>	sp	P08069	IGF1R_HUMAN Insulin-like growth factor 1 receptor prec...	231	3e-60
<input type="checkbox"/>	sp_vs	Q16288-3	Isoform C of Q16288 - Homo sapiens (Human) [NTRK3...	225	2e-58
<input type="checkbox"/>	sp_vs	Q16288-4	Isoform D of Q16288 - Homo sapiens (Human) [NTRK3...	221	3e-57
<input type="checkbox"/>	sp	P06213	INSR_HUMAN Insulin receptor precursor (EC 2.7.10.1) (I...	218	3e-56
<input type="checkbox"/>	tr	Q59H98	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...	218	3e-56
<input type="checkbox"/>	tr	Q17RW0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	218	3e-56
<input type="checkbox"/>	sp_vs	P06213-2	Isoform Short of P06213 - Homo sapiens (Human) [I...	218	3e-56
<input type="checkbox"/>	sp	O15146	MUSK_HUMAN Muscle, skeletal receptor tyrosine protein ...	218	4e-56
<input type="checkbox"/>	tr	Q5VZW8	_HUMAN Muscle, skeletal, receptor tyrosine kinase [MUSK...]	218	4e-56
<input type="checkbox"/>	tr	Q5VZW7	_HUMAN Muscle, skeletal, receptor tyrosine kinase [MUSK...]	218	4e-56
<input type="checkbox"/>	tr	Q32MJ9	_HUMAN MUSK protein [MUSK] [Homo sapiens (Human)]	218	4e-56
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<input type="checkbox"/>	sp	Q16288	NTRK3_HUMAN NT-3 growth factor receptor precursor (EC ...	216	1e-55
<input type="checkbox"/>	sp	P14616	INSRR_HUMAN Insulin receptor-related protein precursor...	213	9e-55
<input type="checkbox"/>	tr	Q5VZS3	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	213	9e-55

[]	sp	Q13308	PTK7_HUMAN Tyrosine-protein kinase-like 7 precursor (C...)	211	5e-54
[]	tr	Q6IQ54	_HUMAN PTK7 protein tyrosine kinase 7 [PTK7] [Homo sapi...	211	5e-54
[]	tr	Q5T650	_HUMAN PTK7 protein tyrosine kinase 7 (PTK7 protein tyr...	211	5e-54
[]	sp	P08922	ROS_HUMAN Proto-oncogene tyrosine-protein kinase ROS p...	210	8e-54
[]	tr	Q5TDB4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	210	8e-54
[]	sp	P04629	NTRK1_HUMAN High affinity nerve growth factor receptor...	209	1e-53
[]	sp	P42679	MATK_HUMAN Megakaryocyte-associated tyrosine-protein k...	209	1e-53
[]	tr	Q9NST8	_HUMAN Putative uncharacterized protein DKFZp434N1212 (...)	209	1e-53
[]	tr	A6NF12	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	209	1e-53
[]	sp_vs	P04629-2	Isoform TrkA-I of P04629 - Homo sapiens (Human) [...]	209	1e-53
[]	sp	Q16620	NTRK2_HUMAN BDNF/NT-3 growth factors receptor precurs...	209	2e-53
[]	tr	Q5VVP4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	209	2e-53
[]	tr	Q8NFA8	_HUMAN Transmembrane receptor PTK7-2 (PTK7 protein tyro...	207	7e-53
[]	sp	Q9UM73	ALK_HUMAN ALK tyrosine kinase receptor precursor (EC 2...	206	1e-52
[]	tr	Q8TDJ5	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	206	1e-52
[]	tr	A6P4V4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	206	1e-52
[]	tr	A6P4T4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	206	1e-52
[]	tr	Q8WXJ7	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...]	206	1e-52
[]	tr	Q8NFA7	_HUMAN Transmembrane receptor PTK7-3 (PTK7 protein tyro...	205	3e-52
[]	sp	P30530	UFO_HUMAN Tyrosine-protein kinase receptor UFO precurs...	204	3e-52
[]	sp	P42684	ABL2_HUMAN Tyrosine-protein kinase ABL2 (EC 2.7.10.2) ...	204	3e-52
[]	tr	A0M8X0	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	204	3e-52
[]	sp_vs	P42684-2	Isoform IA of P42684 - Homo sapiens (Human) [ABL2...]	204	3e-52
[]	sp_vs	P42684-3	Isoform IC of P42684 - Homo sapiens (Human) [ABL2...]	204	3e-52
[]	sp_vs	P42684-4	Isoform 4 of P42684 - Homo sapiens (Human) [ABL2]...	204	3e-52
[]	sp_vs	P30530-2	Isoform Short of P30530 - Homo sapiens (Human) [A...	204	3e-52
[]	sp	P42685	FRK_HUMAN Tyrosine-protein kinase FRK (EC 2.7.10.2) (F...	204	4e-52
[]	sp	P16591	FER_HUMAN Proto-oncogene tyrosine-protein kinase FER (...)	204	4e-52
[]	tr	Q9NTR5	_HUMAN Fyn-related kinase [FRK] [Homo sapiens (Human)]	204	4e-52
[]	tr	Q8N5L2	_HUMAN AXL receptor tyrosine kinase [AXL] [Homo sapiens...]	204	6e-52
[]	sp	P00519	ABL1_HUMAN Proto-oncogene tyrosine-protein kinase ABL1...	203	1e-51
[]	tr	Q59FK4	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
[]	tr	Q17R61	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
[]	tr	A3KFJ3	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
[]	sp_vs	P00519-2	Isoform IB of P00519 - Homo sapiens (Human) [ABL1...]	203	1e-51
[]	tr	Q53EL3	_HUMAN C-src tyrosine kinase variant (Fragment) [Homo s...	202	2e-51
[]	sp	Q9H3Y6	SRMS_HUMAN Tyrosine-protein kinase Srms (EC 2.7.10.2) ...	201	3e-51
[]	tr	Q1RMG3	_HUMAN MERTK protein [MERTK] [Homo sapiens (Human)]	201	4e-51
[]	sp	Q12866	MERTK_HUMAN Proto-oncogene tyrosine-protein kinase MER...	201	5e-51
[]	sp	P41240	CSK_HUMAN Tyrosine-protein kinase CSK (EC 2.7.10.2) (C...)	201	5e-51
[]	tr	Q53R53	_HUMAN Putative uncharacterized protein MERTK (Fragment...)	201	5e-51
[]	sp	P16234	PGFRA_HUMAN Alpha-type platelet-derived growth factor ...	199	1e-50
[]	tr	Q16176	_HUMAN Lsk protein [lsk] [Homo sapiens (Human)]	197	5e-50
[]	tr	Q96T36	_HUMAN Fibroblast growth factor receptor 3 IIIc isoform...	196	9e-50
[]	sp	P08631	HCK_HUMAN Tyrosine-protein kinase HCK (EC 2.7.10.2) (p...)	195	3e-49
[]	sp_vs	P08631-2	Isoform p59-HCK of P08631 - Homo sapiens (Human) ...	195	3e-49
[]	sp	Q06418	TYRO3_HUMAN Tyrosine-protein kinase receptor TYRO3 pre...	194	3e-49
[]	sp	P06239	LCK_HUMAN Proto-oncogene tyrosine-protein kinase LCK (...)	194	3e-49
[]	tr	Q8N6J3	_HUMAN TYRO3 protein (Fragment) [TYRO3] [Homo sapiens (...)	194	3e-49
[]	tr	Q7RTZ3	_HUMAN Protein tyrosine kinase (Lymphocyte-specific pro...)	194	3e-49
[]	tr	Q59FM9	_HUMAN TYRO3 protein tyrosine kinase variant (Fragment)...)	194	3e-49
[]	sp	P34925	RYK_HUMAN Tyrosine-protein kinase RYK precursor (EC 2....)	193	8e-49
[]	tr	Q59F19	_HUMAN Proto-oncogene tyrosine-protein kinase ABL1 vari...	193	1e-48
[]	tr	Q2VXT0	_HUMAN Proto-oncogene c-fes variant 1 [Homo sapiens (Hu...)	193	1e-48
[]	tr	Q2VXS9	_HUMAN Proto-oncogene c-fes variant 3 [Homo sapiens (Hu...)	193	1e-48
[]	tr	Q2VXS7	_HUMAN Proto-oncogene c-fes variant 4 [Homo sapiens (Hu...)	193	1e-48
[]	sp_vs	P34925-2	Isoform 2 of P34925 - Homo sapiens (Human) [RYK] ...	193	1e-48
[]	sp	P07948	LYN_HUMAN Tyrosine-protein kinase Lyn (EC 2.7.10.2) [L...	192	1e-48
[]	tr	Q6NUK7	_HUMAN LYN protein (Fragment) [LYN] [Homo sapiens (Human)]	192	1e-48
[]	sp_vs	P07948-2	Isoform LYN B of P07948 - Homo sapiens (Human) [L...	192	1e-48
[]	tr	Q8WTZ8	_HUMAN RYK protein (Fragment) [RYK] [Homo sapiens (Human)]	192	2e-48
[]	sp	P09619	PGFRB_HUMAN Beta-type platelet-derived growth factor r...	191	3e-48
[]	sp	P07332	FES_HUMAN Proto-oncogene tyrosine-protein kinase Fes/F...	191	3e-48
[]	tr	Q59F04	_HUMAN Platelet-derived growth factor receptor beta var...	191	3e-48
[]	sp	P36888	FLT3_HUMAN FL cytokine receptor precursor (EC 2.7.10.1...)	191	5e-48
[]	tr	Q59EB3	_HUMAN Met proto-oncogene variant (Fragment) [Homo sapi...	191	5e-48

tr	A1L467	_HUMAN Met proto-oncogene (Hepatocyte growth factor rec...	191	5e-48
sp_vs	P21802-14	Isoform 14 of P21802 - Homo sapiens (Human) [FGF...	191	5e-48
tr	Q8NFA6	_HUMAN Transmembrane receptor PTK7-4 (PTK7 protein tyro...	190	6e-48
sp	Q04912	RON_HUMAN Macrophage-stimulating protein receptor prec...	189	1e-47
sp	P08581	MET_HUMAN Hepatocyte growth factor receptor precursor ...	189	1e-47
sp	P29376	LTK_HUMAN Leukocyte tyrosine kinase receptor precursor...	189	1e-47
tr	A6NNJ8	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	189	1e-47
sp_vs	P08581-2	Isoform 2 of P08581 - Homo sapiens (Human) [MET] ...	189	1e-47
sp_vs	Q04912-2	Isoform Delta-RON of Q04912 - Homo sapiens (Human...)	189	1e-47
sp	Q05397	FAK1_HUMAN Focal adhesion kinase 1 (EC 2.7.10.2) (FADK...	188	2e-47
tr	Q8IYN9	_HUMAN PTK2 protein [PTK2] [Homo sapiens (Human)]	188	2e-47
tr	Q658W2	_HUMAN Putative uncharacterized protein DKFZp66600110 [...	188	2e-47
sp	Q16832	DDR2_HUMAN Discoidin domain-containing receptor 2 prec...	188	3e-47
sp	Q01973	ROR1_HUMAN Tyrosine-protein kinase transmembrane recep...	187	4e-47
tr	Q7Z730	_HUMAN Discoidin domain receptor family, member 2 (Disc...	187	4e-47
tr	A2VCQ3	_HUMAN ROR1 protein (Fragment) [ROR1] [Homo sapiens (Hu...	187	4e-47
tr	Q6MZT2	_HUMAN Putative uncharacterized protein DKFZp686D1354 [...	187	5e-47
tr	Q8N9D7	_HUMAN CDNA FLJ37680 fis, clone BRHIP2012923, highly si...	186	9e-47
tr	Q59GN8	_HUMAN PTK2 protein tyrosine kinase 2 isoform b variant...	186	9e-47
tr	Q59GM6	_HUMAN PTK2 protein tyrosine kinase 2 isoform b variant...	186	9e-47
tr	Q12787	_HUMAN Receptor tyrosine kinase (Fragment) [Homo sapien...	186	9e-47
tr	Q5VTU6	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	185	2e-46
sp	Q13882	PTK6_HUMAN Tyrosine-protein kinase 6 (EC 2.7.10.2) (Br...	184	6e-46
sp	Q01974	ROR2_HUMAN Tyrosine-protein kinase transmembrane recep...	183	8e-46
tr	Q5VTT3	_HUMAN Receptor tyrosine kinase-like orphan receptor 2 ...	183	8e-46
tr	A6NNI9	_HUMAN Uncharacterized protein ROR2 [ROR2] [Homo sapien...	183	8e-46
tr	A1L4F5	_HUMAN Receptor tyrosine kinase-like orphan receptor 2 ...	183	8e-46
sp_vs	P06239-3	Isoform 3 of P06239 - Homo sapiens (Human) [LCK] ...	183	8e-46
sp	P12931	SRC_HUMAN Proto-oncogene tyrosine-protein kinase Src (...)	182	2e-45
sp	P51813	BMX_HUMAN Cytoplasmic tyrosine-protein kinase BMX (EC ...)	182	2e-45
tr	Q76P87	_HUMAN V-src sarcoma (Schmidt-Ruppin A-2) viral oncogen...	182	2e-45
sp_vs	P12931-2	Isoform 2 of P12931 - Homo sapiens (Human) [SRC] ...	182	2e-45
sp	P51451	BLK_HUMAN Tyrosine-protein kinase BLK (EC 2.7.10.2) (B...	182	2e-45
tr	Q96IN1	_HUMAN B lymphoid tyrosine kinase (B lymphoid tyrosine ...	182	2e-45
tr	Q96T35	_HUMAN Fibroblast growth factor receptor 3 IIIc isoform...	181	5e-45
tr	Q5R3A8	_HUMAN FYN oncogene related to SRC, FGR, YES [FYN] [Hom...	181	5e-45
tr	A6NIP9	_HUMAN Uncharacterized protein FYN [FYN] [Homo sapiens ...	181	5e-45
tr	Q6NSK4	_HUMAN DDR1 protein [DDR1] [Homo sapiens (Human)]	180	7e-45
tr	A6NP30	_HUMAN Uncharacterized protein PTK7 [PTK7] [Homo sapien...	180	9e-45
sp_vs	P06241-2	Isoform 2 of P06241 - Homo sapiens (Human) [FYN] ...	180	9e-45
sp	Q08345	DDR1_HUMAN Epithelial discoidin domain-containing rece...	179	1e-44
tr	Q5ST11	_HUMAN Discoidin domain receptor family, member 1 (Disc...	179	1e-44
tr	Q573B4	_HUMAN Proto-oncogene tyrosine-protein kinase LCK [LCK]...	179	1e-44
tr	Q4LE50	_HUMAN DDR1 variant protein (Fragment) [DDR1 variant pr...	179	1e-44
tr	Q2L6H3	_HUMAN Discoidin domain receptor family, member 1 (Disc...	179	1e-44
sp_vs	Q08345-2	Isoform 2 of Q08345 - Homo sapiens (Human) [DDR1]...	179	1e-44
sp	P07947	YES_HUMAN Proto-oncogene tyrosine-protein kinase Yes (...)	179	1e-44
sp	P42680	TEC_HUMAN Tyrosine-protein kinase Tec (EC 2.7.10.2) [T...	178	3e-44
tr	A6NIH9	_HUMAN Uncharacterized protein BMX [BMX] [Homo sapiens ...]	178	3e-44
sp	Q15375	EPHA7_HUMAN Ephrin type-A receptor 7 precursor (EC 2.7...	177	4e-44
tr	A6NLB3	_HUMAN Uncharacterized protein YES1 [YES1] [Homo sapien...	177	4e-44
sp_vs	Q15375-2	Isoform 2 of Q15375 - Homo sapiens (Human) [EPHA7...	177	4e-44
sp	P06241	FYN_HUMAN Proto-oncogene tyrosine-protein kinase Fyn (...)	176	1e-43
sp	Q14289	FAK2_HUMAN Protein tyrosine kinase 2 beta (EC 2.7.10.2...)	176	1e-43
sp	P29320	EPHA3_HUMAN Ephrin type-A receptor 3 precursor (EC 2.7...)	176	1e-43
tr	Q6ZRA8	_HUMAN CDNA FLJ46514 fis, clone THYMU3032798, highly si...	176	1e-43
tr	Q6PID4	_HUMAN PTK2B protein tyrosine kinase 2 beta [PTK2B] [Ho...	176	1e-43
tr	Q6P4R6	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA3] [Homo sapi...	176	1e-43
tr	Q59GM4	_HUMAN PTK2B protein tyrosine kinase 2 beta isoform a v...	176	1e-43
sp_vs	Q14289-2	Isoform 2 of Q14289 - Homo sapiens (Human) [PTK2B...]	176	1e-43
sp_vs	Q05397-2	Isoform 2 of Q05397 - Homo sapiens (Human) [PTK2]...	176	1e-43
sp	P04626	ERBB2_HUMAN Receptor tyrosine-protein kinase erbB-2 pr...	176	2e-43
tr	Q05D26	_HUMAN BLK protein (Fragment) [BLK] [Homo sapiens (Human)]	176	2e-43
sp	P09769	FGR_HUMAN Proto-oncogene tyrosine-protein kinase FGR (...)	175	2e-43
sp	Q15303	ERBB4_HUMAN Receptor tyrosine-protein kinase erbB-4 pr...	175	2e-43
sp_vs	Q15303-2	Isoform JM-B of Q15303 - Homo sapiens (Human) [ER...	175	2e-43

<input type="checkbox"/>	sp_vs	Q15303-3	Isoform 3 of Q15303 - Homo sapiens (Human) [ERBB4...]	175	2e-43
<input type="checkbox"/>	sp	P29322	EPHA8_HUMAN Ephrin type-A receptor 8 precursor (EC 2.7...)	175	3e-43
<input type="checkbox"/>	sp_vs	Q05397-3	Isoform 3 of Q05397 - Homo sapiens (Human) [PTK2...]	174	5e-43
<input type="checkbox"/>	sp	P54756	EPHA5_HUMAN Ephrin type-A receptor 5 precursor (EC 2.7...)	174	6e-43
<input type="checkbox"/>	sp	P29317	EPHA2_HUMAN Ephrin type-A receptor 2 precursor (EC 2.7...)	174	6e-43
<input type="checkbox"/>	tr	Q8N3Z2	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA2] [Homo sapi...]	174	6e-43
<input type="checkbox"/>	tr	Q59FT4	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [Homo s...]	174	6e-43
<input type="checkbox"/>	tr	A2ARL4	_HUMAN Discoidin domain receptor family, member 1 (Frag...)	174	6e-43
<input type="checkbox"/>	sp_vs	P54756-2	Isoform 2 of P54756 - Homo sapiens (Human) [EPHA5...]	174	6e-43
<input type="checkbox"/>	sp	P54764	EPHA4_HUMAN Ephrin type-A receptor 4 precursor (EC 2.7...)	171	3e-42
<input type="checkbox"/>	sp	P21709	EPHA1_HUMAN Ephrin type-A receptor 1 precursor (EC 2.7...)	171	3e-42
<input type="checkbox"/>	tr	Q58F15	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA4] [Homo sapi...]	171	3e-42
<input type="checkbox"/>	tr	Q53TA0	_HUMAN Putative uncharacterized protein EPHA4 (Fragment...)	171	3e-42
<input type="checkbox"/>	tr	A1L3V3	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA1] [Homo sapi...]	171	3e-42
<input type="checkbox"/>	tr	Q9NSQ6	_HUMAN Putative uncharacterized protein DKFZp434L0319 (...)	171	5e-42
<input type="checkbox"/>	tr	Q7Z3F2	_HUMAN Ephrin receptor (EC 2.7.10.1) [DKFZp686C0686] [H...]	171	5e-42
<input type="checkbox"/>	sp	P29323	EPHB2_HUMAN Ephrin type-B receptor 2 precursor (EC 2.7...)	169	2e-41
<input type="checkbox"/>	tr	Q5TFU3	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB2] [Homo sapi...]	169	2e-41
<input type="checkbox"/>	tr	Q4LE53	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [EPHB2 ...]	169	2e-41
<input type="checkbox"/>	tr	A6NJMO	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB2] [Homo sapi...]	169	2e-41
<input type="checkbox"/>	sp_vs	P29323-2	Isoform 2 of P29323 - Homo sapiens (Human) [EPHB2...]	169	2e-41
<input type="checkbox"/>	sp_vs	P29323-3	Isoform 3 of P29323 - Homo sapiens (Human) [EPHB2...]	169	2e-41
<input type="checkbox"/>	sp	Q06187	BTK_HUMAN Tyrosine-protein kinase BTK (EC 2.7.10.2) (B...)	169	2e-41
<input type="checkbox"/>	sp	P00533	EGFR_HUMAN Epidermal growth factor receptor precursor ...	168	3e-41
<input type="checkbox"/>	tr	Q59FL8	_HUMAN Epidermal growth factor receptor isoform a varia...	168	3e-41
<input type="checkbox"/>	tr	Q504U8	_HUMAN EGFR protein [EGFR] [Homo sapiens (Human)]	168	3e-41
<input type="checkbox"/>	tr	Q2TTR7	_HUMAN Cell growth inhibiting protein 40 [Homo sapiens ...]	168	3e-41
<input type="checkbox"/>	tr	Q4JFK8	_HUMAN Fes/fps proto-oncogene (Fragment) [FES] [Homo sa...]	168	3e-41
<input type="checkbox"/>	tr	Q59GQ2	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) (Fragment...)	167	4e-41
<input type="checkbox"/>	sp	P42681	TXK_HUMAN Tyrosine-protein kinase TXK (EC 2.7.10.2) [T...]	167	6e-41
<input type="checkbox"/>	sp	O60674	JAK2_HUMAN Tyrosine-protein kinase JAK2 (EC 2.7.10.2) ...	166	1e-40
<input type="checkbox"/>	tr	Q8IXP2	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK2] [Ho...]	166	1e-40
<input type="checkbox"/>	tr	Q506QC	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK2] [Ho...]	166	1e-40
<input type="checkbox"/>	sp	P54762	EPHB1_HUMAN Ephrin type-B receptor 1 precursor (EC 2.7...)	166	1e-40
<input type="checkbox"/>	sp_vs	P54762-2	Isoform 2 of P54762 - Homo sapiens (Human) [EPHB1...]	166	1e-40
<input type="checkbox"/>	tr	Q0VG87	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB1] [Homo sapi...]	165	3e-40
<input type="checkbox"/>	sp	P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 (EC 2.7.10.2) ...	164	4e-40
<input type="checkbox"/>	sp	P43405	KSYK_HUMAN Tyrosine-protein kinase SYK (EC 2.7.10.2) (...)	164	6e-40
<input type="checkbox"/>	tr	Q5T6N8	_HUMAN Spleen tyrosine kinase (Spleen tyrosine kinase, ...)	164	6e-40
<input type="checkbox"/>	tr	Q5T6N7	_HUMAN Spleen tyrosine kinase (Spleen tyrosine kinase, ...)	164	6e-40
<input type="checkbox"/>	tr	Q59FQ5	_HUMAN RYK receptor-like tyrosine kinase isoform 1 vari...	164	6e-40
<input type="checkbox"/>	sp_vs	P43405-2	Isoform Short of P43405 - Homo sapiens (Human) [S...]	164	6e-40
<input type="checkbox"/>	sp	P54760	EPHB4_HUMAN Ephrin type-B receptor 4 precursor (EC 2.7...)	163	8e-40
<input type="checkbox"/>	tr	Q96L35	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...]	163	8e-40
<input type="checkbox"/>	tr	Q7Z635	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...]	163	8e-40
<input type="checkbox"/>	tr	Q59F17	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [Homo s...]	163	8e-40
<input type="checkbox"/>	tr	Q541P7	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...]	163	8e-40
<input type="checkbox"/>	sp	Q08881	ITK_HUMAN Tyrosine-protein kinase ITK/TSK (EC 2.7.10.2...)	163	1e-39
<input type="checkbox"/>	tr	Q9UMB0	_HUMAN Fibroblast growth factor receptor-related protei...	162	1e-39
<input type="checkbox"/>	tr	Q9H7V3	_HUMAN CDNA FLJ14219 fis, clone NT2RP3003800, highly si...	162	2e-39
<input type="checkbox"/>	sp	P43403	ZAP70_HUMAN Tyrosine-protein kinase ZAP-70 (EC 2.7.10....)	160	5e-39
<input type="checkbox"/>	tr	Q6PIA4	_HUMAN ZAP70 protein (Putative uncharacterized protein ...)	160	5e-39
<input type="checkbox"/>	sp	P54753	EPHB3_HUMAN Ephrin type-B receptor 3 precursor (EC 2.7...)	160	7e-39
<input type="checkbox"/>	sp_vs	P06241-3	Isoform 3 of P06241 - Homo sapiens (Human) [FYNN] ...	160	9e-39
<input type="checkbox"/>	sp_vs	Q01973-2	Isoform Short of Q01973 - Homo sapiens (Human) [R...]	160	9e-39
<input type="checkbox"/>	sp	Q6J9G0	STYK1_HUMAN Tyrosine protein-kinase STYK1 (EC 2.7.10.2...)	158	4e-38
<input type="checkbox"/>	sp	Q07912	ACK1_HUMAN Activated CDC42 kinase 1 (EC 2.7.10.2) (ACK...)	156	1e-37
<input type="checkbox"/>	tr	Q6ZMQ0	_HUMAN CDNA FLJ16772 fis, clone BRAWH3043827, highly si...	156	1e-37
<input type="checkbox"/>	sp_vs	Q07912-2	Isoform 2 of Q07912 - Homo sapiens (Human) [TNK2]...	156	1e-37
<input type="checkbox"/>	sp	P29597	TYK2_HUMAN Non-receptor tyrosine-protein kinase TYK2 (...)	155	2e-37
<input type="checkbox"/>	tr	Q2VKS9	_HUMAN Proto-oncogene c-fes variant 2 [Homo sapiens (Hu...)	155	2e-37
<input type="checkbox"/>	tr	Q8IXD6	_HUMAN Truncated ZAP kinase [Homo sapiens (Human)]	155	2e-37
<input type="checkbox"/>	tr	Q6LBK2	_HUMAN Acidic fibroblast growth factor (Fragment) [FGFR...]	155	2e-37
<input type="checkbox"/>	tr	Q4LDX3	_HUMAN Janus kinase 1 [JAK1] [Homo sapiens (Human)]	154	5e-37
<input type="checkbox"/>	tr	Q96T34	_HUMAN Fibroblast growth factor receptor 3 IIIc isoform...	154	7e-37
<input type="checkbox"/>	tr	A6NFP4	_HUMAN Uncharacterized protein ZAP70 [ZAP70] [Homo sapi...]	154	7e-37

tr	Q53T57	_HUMAN Putative uncharacterized protein ERBB4 (Fragment...)	152	2e-36
sp	P52333	JAK3_HUMAN Tyrosine-protein kinase JAK3 (EC 2.7.10.2) ...	152	3e-36
tr	Q99699	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK3] [Ho...]	152	3e-36
tr	Q75MF2	_HUMAN Putative uncharacterized protein EGFR (Fragment...)	150	1e-35
tr	Q59FX1	_HUMAN Putative uncharacterized protein (Fragment) [Hom...]	150	1e-35
sp	P21860	ERBB3_HUMAN Receptor tyrosine-protein kinase erbB-3 pr...	148	4e-35
tr	Q15516	_HUMAN Tyrosine kinase [Homo sapiens (Human)]	147	6e-35
sp	Q5JZY3	EPHAA_HUMAN Ephrin type-A receptor 10 precursor (EC 2....)	145	2e-34
tr	Q3MS96	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	145	2e-34
sp	Q9UF33	EPHA6_HUMAN Ephrin type-A receptor 6 precursor (EC 2.7....)	144	7e-34
tr	Q6ZNH1	_HUMAN CDNA FLJ16103 fis, clone TESTI2016663, moderate...	144	7e-34
sp_vs	P54762-3	Isoform 3 of P54762 - Homo sapiens (Human) [EPHB1...]	142	3e-33
tr	Q96HF4	_HUMAN EPHA2 protein (Fragment) [EPHA2] [Homo sapiens (...]	141	3e-33
sp	Q96Q04	LMTK3_HUMAN Serine/threonine-protein kinase LMTK3 prec...	135	2e-31
sp	Q12852	M3K12_HUMAN Mitogen-activated protein kinase kinase ki...	134	5e-31
sp	Q8N441	FGRL1_HUMAN Fibroblast growth factor receptor-like 1 p...	133	9e-31
tr	Q9POL3	_HUMAN Bruton's tyrosine kinase (Fragment) [Homo sapien...]	133	9e-31
tr	Q6ZMD4	_HUMAN CDNA FLJ23990 fis, clone HRC08053, highly simila...	133	9e-31
tr	A4FU89	_HUMAN EPHA10 protein [EPHA10] [Homo sapiens (Human)]	132	2e-30
sp_vs	Q5JZY3-3	Isoform 3 of Q5JZY3 - Homo sapiens (Human) [EPHA1...]	132	2e-30
tr	Q3MS92	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	132	3e-30
tr	Q9POL5	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	131	5e-30
sp_vs	P52333-2	Isoform 1 of P52333 - Homo sapiens (Human) [JAK3]...	131	5e-30
sp_vs	P52333-3	Isoform 3 of P52333 - Homo sapiens (Human) [JAK3]...	131	5e-30
sp	Q13470	TNK1_HUMAN Non-receptor tyrosine-protein kinase TNK1 (...)	130	8e-30
tr	Q9POL7	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	8e-30
tr	Q9PGL6	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	8e-30
sp_vs	Q13470-2	Isoform 2 of Q13470 - Homo sapiens (Human) [TNK1]...	130	8e-30
tr	Q9NPI3	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	1e-29
tr	Q9NPI2	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	1e-29
sp	Q9NYL2	MLTK_HUMAN Mitogen-activated protein kinase kinase kin...	129	2e-29
sp	O43283	M3K13_HUMAN Mitogen-activated protein kinase kinase ki...	129	2e-29
sp_vs	Q9NYL2-2	Isoform 2 of Q9NYL2 - Homo sapiens (Human) [MLTK]...	129	2e-29
sp_vs	Q9NYL2-3	Isoform 3 of Q9NYL2 - Homo sapiens (Human) [MLTK]...	129	2e-29
tr	Q59GJ1	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...)	129	2e-29
sp	Q02779	M3K10_HUMAN Mitogen-activated protein kinase kinase ki...	128	4e-29
sp	P80192	M3K9_HUMAN Mitogen-activated protein kinase kinase kin...	127	5e-29
tr	A3KN85	_HUMAN MAP3K9 protein [MAP3K9] [Homo sapiens (Human)]	127	5e-29
sp_vs	P80192-4	Isoform 2 of P80192 - Homo sapiens (Human) [MAP3K...]	127	5e-29
sp	Q6ZMQ8	LMTK1_HUMAN Serine/threonine-protein kinase LMTK1 (EC ...)	124	4e-28
tr	Q6P4HS	_HUMAN PDGFRA protein [PDGFRA] [Homo sapiens (Human)]	124	4e-28
sp_vs	Q6ZMQ8-3	Isoform 3 of Q6ZMQ8 - Homo sapiens (Human) [AATK]...	124	4e-28
sp	Q5TCX8	M3KL4_HUMAN Mitogen-activated protein kinase kinase ki...	123	1e-27
sp	Q16584	M3K11_HUMAN Mitogen-activated protein kinase kinase ki...	123	1e-27
sp_vs	Q5TCX8-2	Isoform 2 of Q5TCX8 - Homo sapiens (Human) [MLK4]...	123	1e-27
sp	O15197	EPHB6_HUMAN Ephrin type-B receptor 6 precursor (Tyrosi...	122	2e-27
tr	Q2TB24	_HUMAN EPHB6 protein (EPH receptor B6, isoform CRA_b) [...]	122	2e-27
tr	Q2TB23	_HUMAN EPH receptor B6 (EphB6) [EPHB6] [Homo sapiens (H...]	122	2e-27
tr	Q9UMA9	_HUMAN Fibroblast growth factor receptor (Fragment) [BE...]	122	3e-27
tr	Q9POM0	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	121	4e-27
sp	O43318	M3K7_HUMAN Mitogen-activated protein kinase kinase ki...	113	1e-24
tr	Q9NZ70	_HUMAN TGF beta-activated kinase splice variant d (Mito...)	113	1e-24
tr	Q5U0D0	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	113	1e-24
tr	Q5TDM9	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	113	1e-24
sp_vs	O43318-2	Isoform 1A of O43318 - Homo sapiens (Human) [MAP3...]	113	1e-24
sp_vs	O43318-3	Isoform 1C of O43318 - Homo sapiens (Human) [MAP3...]	113	1e-24
tr	Q5U0C9	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	112	2e-24
tr	Q5JY90	_HUMAN Bruton agammaglobulinemia tyrosine kinase (Bruto...)	110	8e-24
sp	P04049	RAF1_HUMAN RAF proto-oncogene serine/threonine-protein...	104	5e-22
tr	Q59HE0	_HUMAN Colony stimulating factor 1 receptor variant (Fr...)	104	5e-22
tr	Q15278	_HUMAN RAF1 protein (Fragment) [RAF1] [Homo sapiens (Hu...]	104	5e-22
sp	Q13546	RIPK1_HUMAN Receptor-interacting serine/threonine-prot...	103	8e-22
sp	Q8IWU2	LMTK2_HUMAN Serine/threonine-protein kinase LMTK2 prec...	103	1e-21
tr	A4D272	_HUMAN Lemur tyrosine kinase 2 (Lemur tyrosine kinase 2...)	103	1e-21
sp	P15056	BRAF1_HUMAN B-Raf proto-oncogene serine/threonine-prot...	102	2e-21
tr	Q5IBP5	_HUMAN AKAP9-BRAF fusion protein [Homo sapiens (Human)]	102	2e-21

[]	tr	A4D1T4	_HUMAN V-raf murine sarcoma viral oncogene homolog B1 [...]	102	2e-21
[]	tr	Q5UBV6	_HUMAN NIN/PDGFRB fusion protein (Fragment) [NIN/PDGFRB...]	102	3e-21
[]	sp	P53667	LIMK1_HUMAN LIM domain kinase 1 (EC 2.7.11.1) (LIMK-1)... Isoform 2 of P53667 - Homo sapiens (Human) [LIMK1...]	101	5e-21
[]	sp_vs	P53667-2	Isoform 2 of P53667 - Homo sapiens (Human) [LIMK1...]	101	5e-21
[]	sp	P10398	ARAF_HUMAN A-Raf proto-oncogene serine/threonine-prote...	100	7e-21
[]	tr	Q96II15	_HUMAN ARAF protein [ARAF] [Homo sapiens (Human)]	100	7e-21
[]	tr	Q8TCG9	_HUMAN KIT protein (Fragment) [KIT] [Homo sapiens (Human)]	100	9e-21
[]	sp	Q96S53	TESK2_HUMAN Dual specificity testis-specific protein k...	99	2e-20
[]	tr	Q5T152	_HUMAN Testis-specific kinase 2 (Testis-specific kinase...)	99	2e-20
[]	sp	Q9Y6E0	STK24_HUMAN Serine/threonine-protein kinase 24 (EC 2.7...)	99	3e-20
[]	tr	Q6P0Y1	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...)	99	3e-20
[]	tr	Q5U0E6	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...)	99	3e-20
[]	tr	Q5T5B3	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...)	99	3e-20
[]	tr	A0PJ49	_HUMAN FGFR1 protein (Fragment) [FGFR1] [Homo sapiens...]	99	3e-20
[]	sp_vs	Q9Y6E0-2	Isoform A of Q9Y6E0 - Homo sapiens (Human) [STK24...]	99	3e-20
[]	sp	Q04759	KPCT_HUMAN Protein kinase C theta type (EC 2.7.11.13) ...	98	4e-20
[]	tr	Q9UDF1	_HUMAN Fibroblast growth factor receptor 1 THIRD immuno...	98	4e-20
[]	tr	Q5JUN8	_HUMAN Protein kinase C, theta (Fragment) [PRKCQ] [Homo...]	98	4e-20
[]	sp	QGP3R8	NEK5_HUMAN Serine/threonine-protein kinase Nek5 (EC 2....)	97	1e-19
[]	tr	Q6FG81	_HUMAN STK24 protein (Fragment) [STK24] [Homo sapiens (...)	97	1e-19
[]	tr	A6NIT1	_HUMAN Uncharacterized protein ARAF [ARAF] [Homo sapien...]	96	2e-19
[]	sp	Q15418	KS6A1_HUMAN Ribosomal protein S6 kinase alpha-1 (EC 2....)	95	4e-19
[]	tr	A6NGG4	_HUMAN Uncharacterized protein RPS6KA1 [RPS6KA1] [Homo ...]	95	4e-19
[]	tr	A6NFC2	_HUMAN Uncharacterized protein ERBB2 [ERBB2] [Homo sapi...]	95	5e-19
[]	sp	Q9H2G2	SLK_HUMAN STE20-like serine/threonine-protein kinase (...)	94	8e-19
[]	sp	Q9P0L2	MARK1_HUMAN Serine/threonine-protein kinase MARK1 (EC ...)	94	8e-19
[]	sp_vs	Q9H2G2-2	Isoform 2 of Q9H2G2 - Homo sapiens (Human) [SLK] ...	94	8e-19
[]	sp_vs	P27448-3	Isoform 3 of P27448 - Homo sapiens (Human) [MARK3...]	94	1e-18
[]	sp_vs	P27448-4	Isoform 4 of P27448 - Homo sapiens (Human) [MARK3...]	94	1e-18
[]	sp_vs	P27448-5	Isoform 5 of P27448 - Homo sapiens (Human) [MARK3...]	94	1e-18
[]	sp_vs	P27448-6	Isoform 6 of P27448 - Homo sapiens (Human) [MARK3...]	94	1e-18
[]	tr	Q14219	_HUMAN Protein tyrosine kinase (Fragment) [tec] [Homo s...]	93	1e-18
[]	sp	Q7KZI7	MARK2_HUMAN Serine/threonine-protein kinase MARK2 (EC ...)	93	2e-18
[]	sp_vs	Q7KZI7-2	Isoform 2 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-3	Isoform 3 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-4	Iscform 4 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-5	Isoform 5 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-6	Isoform 6 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-7	Isoform 7 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-8	Isoform 8 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-9	Isoform 9 of Q7KZI7 - Homo sapiens (Human) [MARK2...]	93	2e-18
[]	sp_vs	Q7KZI7-10	Isoform 10 of Q7KZI7 - Homo sapiens (Human) [MAR...]	93	2e-18
[]	sp_vs	Q7KZI7-11	Isoform 11 of Q7KZI7 - Homo sapiens (Human) [MAR...]	93	2e-18
[]	sp_vs	Q7KZI7-12	Isoform 12 of Q7KZI7 - Homo sapiens (Human) [MAR...]	93	2e-18
[]	sp	Q15569	TESK1_HUMAN Dual specificity testis-specific protein k...	92	3e-18
[]	tr	Q8IXZ8	_HUMAN TESK1 protein (Testis-specific kinase 1, isoform...)	92	3e-18
[]	tr	Q59FZ4	_HUMAN Serine/threonine kinase 4 variant (Fragment) [Ho...]	92	3e-18
[]	sp	Q8TDX7	NEK7_HUMAN Serine/threonine-protein kinase Nek7 (EC 2....)	91	5e-18
[]	sp	P05771	KPCB_HUMAN Protein kinase C beta type (EC 2.7.11.13) (...)	91	5e-18
[]	tr	A6NH24	_HUMAN Uncharacterized protein ROBO1 [ROBO1] [Homo sapi...]	91	5e-18
[]	sp_vs	P05771-2	Isoform Beta-II of P05771 - Homo sapiens (Human) ...	91	5e-18
[]	sp	Q15349	KS6A2_HUMAN Ribosomal protein S6 kinase alpha-2 (EC 2....)	91	7e-18
[]	tr	Q05DF6	_HUMAN NEK4 protein (Fragment) [NEK4] [Homo sapiens (Hu...]	91	7e-18
[]	tr	A6NNND1	_HUMAN Uncharacterized protein RPS6KA2 [RPS6KA2] [Homo ...]	91	7e-18
[]	sp_vs	Q05397-4	Isoform 4 of Q05397 - Homo sapiens (Human) [PTK2]...	91	7e-18
[]	sp_vs	Q15349-2	Isoform 2 of Q15349 - Homo sapiens (Human) [RPS6K...]	91	7e-18
[]	sp	Q9Y6N7	ROBO1_HUMAN Roundabout homolog 1 precursor (H-Robo-1) ...	91	9e-18
[]	sp	P51957	NEK4_HUMAN Serine/threonine-protein kinase Nek4 (EC 2....)	91	9e-18
[]	sp	P51812	KS6A3_HUMAN Ribosomal protein S6 kinase alpha-3 (EC 2....)	91	9e-18
[]	tr	Q6P576	_HUMAN NEK4 protein [Homo sapiens (Human)]	91	9e-18
[]	sp_vs	Q9Y6N7-2	Isoform 2 of Q9Y6N7 - Homo sapiens (Human) [ROBO1...]	91	9e-18
[]	sp	Q9UEW8	STK39_HUMAN STE20/SPS1-related proline-alanine-rich pr...	90	1e-17
[]	tr	Q53S90	_HUMAN Putative uncharacterized protein STK39 (Fragment...)	90	1e-17
[]	sp	P27448	MARK3_HUMAN MAP/microtubule affinity-regulating kinase...	90	2e-17
[]	sp_vs	P27448-2	Isoform 2 of P27448 - Homo sapiens (Human) [MARK3...]	90	2e-17
[]	sp_vs	P27448-7	Isoform 7 of P27448 - Homo sapiens (Human) [MARK3...]	90	2e-17

□	tr	Q8NFJ4	_HUMAN Testis-specific kinase-1 (Fragment) [Homo sapien...	89	2e-17
□	tr	Q6NSK0	_HUMAN Serine/threonine kinase 10 [STK10] [Homo sapiens...	89	2e-17
□	tr	Q2M1J3	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89	2e-17
□	tr	Q1RMC8	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89	2e-17
□	tr	Q1RMC7	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89	2e-17
□	sp_vs	Q9Y6N7-3	Isoform 3 of Q9Y6N7 - Homo sapiens (Human) [ROBO1...	89	2e-17
□	sp	Q9H0K1	SNFL2_HUMAN Serine/threonine-protein kinase SNF1-like ...	89	3e-17
□	sp	Q9H093	NUAK2_HUMAN NUAK family SNF1-like kinase 2 (EC 2.7.11....	89	3e-17
□	sp	Q9P289	MST4_HUMAN Serine/threonine-protein kinase MST4 (EC 2....	89	3e-17
□	tr	Q8NBV1	_HUMAN CDNA FLJ90669 fis, clone PLACE1005519, moderate...	89	3e-17
□	tr	Q499L9	_HUMAN Serine/threonine protein kinase MST4 [MST4] [Hom...	89	3e-17
□	sp	Q9NRP7	STK36_HUMAN Serine/threonine-protein kinase 36 (EC 2.7...	89	3e-17
□	sp	P51956	NEK3_HUMAN Serine/threonine-protein kinase Nek3 (EC 2....	89	3e-17
□	tr	Q6ZN64	_HUMAN CDNA FLJ16392 fis, clone TRACH2020048, moderate...	89	3e-17
□	tr	Q5TAP2	_HUMAN NIMA (Never in mitosis gene a)-related kinase 3 ...	89	3e-17
□	tr	Q5T153	_HUMAN Testis-specific kinase 2 [TESK2] [Homo sapiens (...	89	3e-17
□	tr	P78483	_HUMAN C-src-2 protein (Fragment) [FGR] [Homo sapiens (...	89	3e-17
□	tr	ASYM70	_HUMAN NEK4 protein [NEK4] [Homo sapiens (Human)]	89	3e-17
□	sp_vs	Q9NRP7-2	Isoform 2 of Q9NRP7 - Homo sapiens (Human) [STK36...	89	3e-17
□	sp_vs	Q96S53-3	Isoform 3 of Q96S53 - Homo sapiens (Human) [TESK2...	89	3e-17
□	tr	Q9UEH2	_HUMAN BEK fibroblast growth factor receptor (Fragment)...	88	4e-17
□	tr	Q8J023	_HUMAN NIMA-related protein kinase 3 [NEK3] [Homo sapie...	88	4e-17
□	tr	Q572P5	_HUMAN Tyrosine-protein kinase BTK isoform 65 (Fragment...	88	4e-17
□	tr	Q08AF4	_HUMAN PKN2 protein [PKN2] [Homo sapiens (Human)]	88	4e-17
□	sp	Q13043	STK4_HUMAN Serine/threonine-protein kinase 4 (EC 2.7.1...	88	6e-17
□	sp	Q94804	STK10_HUMAN Serine/threonine-protein kinase 10 (EC 2.7...	88	6e-17
□	sp	P53671	LIMK2_HUMAN LIM domain kinase 2 (EC 2.7.11.1) (LIMK-2)...	88	6e-17
□	tr	Q9UFU0	_HUMAN Putative uncharacterized protein DKFZp586K0922 (...)	88	6e-17
□	tr	A6ND35	_HUMAN Uncharacterized protein STK10 [STK10] [Homo sapi...	88	6e-17
□	tr	A0PJ51	_HUMAN STK4 protein (Fragment) [STK4] [Homo sapiens (Hu...	88	6e-17
□	sp_vs	P53671-2	Isoform LIMK2b of P53671 - Homo sapiens (Human) [...]	88	6e-17
□	sp_vs	Q13043-2	Isoform 2 of Q13043 - Homo sapiens (Human) [STK4]...	88	6e-17
□	sp	Q16513	PKN2_HUMAN Serine/threonine-protein kinase N2 (EC 2.7....	87	8e-17
□	sp	Q96PY6	NEK1_HUMAN Serine/threonine-protein kinase Nek1 (EC 2....	87	8e-17
□	sp	Q96RW7	HMCN1_HUMAN Hemicentin-1 precursor (Fibulin-6) (FIBL-6...)	87	8e-17
□	tr	Q86XJ6	_HUMAN Protein kinase C, delta (Protein kinase C, delta...	87	8e-17
□	tr	Q14CB7	_HUMAN NEK1 protein [NEK1] [Homo sapiens (Human)]	87	8e-17
□	tr	Q05DG5	_HUMAN NEK1 protein (Fragment) [NEK1] [Homo sapiens (Hu...	87	8e-17
□	tr	A6NGE3	_HUMAN Uncharacterized protein HMCN1 [HMCN1] [Homo sapi...	87	8e-17
□	sp_vs	Q96RW7-2	Isoform 2 of Q96RW7 - Homo sapiens (Human) [HMCN1...]	87	8e-17
□	sp_vs	Q96PY6-2	Isoform 2 of Q96PY6 - Homo sapiens (Human) [NEK1]...	87	8e-17
□	sp_vs	Q13153-2	Isoform 2 of Q13153 - Homo sapiens (Human) [PAK1]...	87	8e-17
□	sp	Q05655	KPCD_HUMAN Protein kinase C delta type (EC 2.7.11.13) ...	87	1e-16
□	sp	Q00526	CDK3_HUMAN Cell division protein kinase 3 (EC 2.7.11.2...)	87	1e-16
□	tr	Q5JPB0	_HUMAN Putative uncharacterized protein DKFZp434B079 [D...	87	1e-16
□	tr	Q5H9T1	_HUMAN Putative uncharacterized protein DKFZp686D06121 ...	87	1e-16
□	sp	Q96L34	MARK4_HUMAN MAP/microtubule affinity-regulating kinase...	87	1e-16
□	sp	Q9UQB9	AURKC_HUMAN Serine/threonine-protein kinase 13 (EC 2.7...	87	1e-16
□	sp_vs	Q96L34-2	Isoform 2 of Q96L34 - Homo sapiens (Human) [MARK4...]	87	1e-16
□	sp	P17252	KPCA_HUMAN Protein kinase C alpha type (EC 2.7.11.13) ...	86	2e-16
□	tr	Q2TSD3	_HUMAN Aging-associated gene 6 protein [Homo sapiens (H...	86	2e-16
□	tr	Q5T5B4	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...)	86	2e-16
□	sp	O14965	STK6_HUMAN Serine/threonine-protein kinase 6 (EC 2.7.1...)	86	3e-16
□	sp	Q13188	STK3_HUMAN Serine/threonine-protein kinase 3 (EC 2.7.1...)	85	4e-16
□	sp	O95747	OXSR1_HUMAN Serine/threonine-protein kinase OSR1 (EC 2...	85	4e-16
□	sp	O60265	NUAK1_HUMAN NUAK family SNF1-like kinase 1 (EC 2.7.11....)	85	4e-16
□	tr	Q6ZNR9	_HUMAN CDNA FLJ27266 fis, clone TMS00356, highly simila...	85	4e-16
□	tr	A7MD39	_HUMAN NUAK family, SNF1-like kinase, 1 (NUAK family, S...	85	4e-16
□	sp	O00506	STK25_HUMAN Serine/threonine-protein kinase 25 (EC 2.7...	84	6e-16
□	sp	Q9HC98	NEK6_HUMAN Serine/threonine-protein kinase Nek6 (EC 2....)	84	6e-16
□	sp	P06493	CDC2_HUMAN Cell division control protein 2 homolog (EC...	84	6e-16
□	tr	Q96BA2	_HUMAN STK25 protein [Homo sapiens (Human)]	84	6e-16
□	tr	Q6FG86	_HUMAN NEK6 protein (Fragment) [NEK6] [Homo sapiens (Hu...	84	6e-16
□	tr	Q5VZ16	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	84	6e-16
□	tr	Q5VZ09	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	84	6e-16
□	sp	Q59H18	TNNI3K_HUMAN Serine/threonine-protein kinase TNNI3K (EC...	84	8e-16

tr	Q6DLZ0	_HUMAN Aurora/Ipl1-related kinase 3 transcript variant ...	84	8e-16
tr	Q6AZY8	_HUMAN AURKC protein (Aurora kinase C, isoform CRA_a) [...]	84	8e-16
tr	Q5Y191	_HUMAN Aurora-C [AURKC] [Homo sapiens (Human)]	84	8e-16
tr	Q3B785	_HUMAN CDC2 protein [CDC2] [Homo sapiens (Human)]	84	8e-16
tr	Q17RNO	_HUMAN TNNI3 interacting kinase [TNNI3K] [Homo sapiens ...]	84	8e-16
sp_vs	Q9UQB9-2	Isoform 2 of Q9UQB9 - Homo sapiens (Human) [AURKC...]	84	8e-16
sp_vs	Q59H18-2	Isoform 2 of Q59H18 - Homo sapiens (Human) [TNNI3...]	84	8e-16
sp	O94779	CNTN5_HUMAN Contactin-5 precursor (Neural recognition ...)	84	1e-15
tr	Q49AF3	_HUMAN CNTN5 protein [CNTN5] [Homo sapiens (Human)]	84	1e-15
tr	A1L4P0	_HUMAN CNTN5 protein [CNTN5] [Homo sapiens (Human)]	84	1e-15
sp_vs	O94779-2	Isoform 2 of O94779 - Homo sapiens (Human) [CNTN5...]	84	1e-15
sp_vs	Q9BYT3-2	Isoform 2 of Q9BYT3 - Homo sapiens (Human) [STK33...]	84	1e-15
sp	Q56UN5	YSK4_HUMAN SPS1/STE20-related protein kinase YSK4 (EC ...)	83	1e-15
sp	Q14680	MELK_HUMAN Maternal embryonic leucine zipper kinase (E...)	83	1e-15
tr	Q5T263	_HUMAN Maternal embryonic leucine zipper kinase (Matern...)	83	1e-15
tr	Q53GX0	_HUMAN Maternal embryonic leucine zipper kinase variant...	83	1e-15
sp_vs	Q56UN5-3	Isoform 3 of Q56UN5 - Homo sapiens (Human) [YSK4]...	83	1e-15
sp_vs	Q56UN5-5	Isoform 5 of Q56UN5 - Homo sapiens (Human) [YSK4]...	83	1e-15
sp	Q00534	CDK6_HUMAN Cell division protein kinase 6 (EC 2.7.11.2...)	83	2e-15
tr	Q5H9N4	_HUMAN Putative uncharacterized protein DKFZp686L20222 ...	83	2e-15
tr	A4D1G0	_HUMAN Cyclin-dependent kinase 6 (HCG19542) [CDK6] [Hom...]	83	2e-15
sp	Q96GD4	AURKB_HUMAN Serine/threonine-protein kinase 12 (EC 2.7...)	82	2e-15
tr	Q6IAR3	_HUMAN NEK6 protein [NEK6] [Homo sapiens (Human)]	82	2e-15
tr	A3KEJ0	_HUMAN Aurora kinase A [AURKA] [Homo sapiens (Human)]	82	2e-15
tr	A2ABM8	_HUMAN Discoidin domain receptor family, member 1 (Frag...)	82	2e-15
tr	A2ABL3	_HUMAN Discoidin domain receptor family, member 1 (Frag...)	82	2e-15
sp	Q6P5Z2	PKN3_HUMAN Serine/threonine-protein kinase N3 (EC 2.7....)	82	3e-15
tr	Q86VSI	_HUMAN Protein kinase, AMP-activated, alpha 1 catalytic...	82	3e-15
tr	Q7L3H5	_HUMAN LIM domain kinase 2 (LIM domain kinase 2, isofor...)	82	3e-15
sp	P57059	SN1L1_HUMAN Serine/threonine-protein kinase SNF1-like ...	82	4e-15
sp	Q6ZN16	M3K15_HUMAN Mitogen-activated protein kinase kinase ki...	82	4e-15
sp	Q13131	AAPK1_HUMAN 5'-AMP-activated protein kinase catalytic ...	82	4e-15
sp_vs	Q6ZN16-2	Isoform 2 of Q6ZN16 - Homo sapiens (Human) [MAP3K...]	82	4e-15
sp_vs	Q6ZN16-3	Isoform 3 of Q6ZN16 - Homo sapiens (Human) [MAP3K...]	82	4e-15
sp	Q16512	PKN1_HUMAN Serine/threonine-protein kinase N1 (EC 2.7....)	81	5e-15
sp	Q13177	PAK2_HUMAN Serine/threonine-protein kinase PAK 2 (EC 2...)	81	5e-15
sp_vs	Q9UPZ9-2	Isoform 2 of Q9UPZ9 - Homo sapiens (Human) [ICK] ...	81	5e-15
sp	Q9H4B4	PLK3_HUMAN Serine/threonine-protein kinase PLK3 (EC 2....)	81	7e-15
sp	Q8NG66	NEK11_HUMAN Serine/threonine-protein kinase Nek11 (EC ...)	81	7e-15
sp	Q9UK32	KS6A6_HUMAN Ribosomal protein S6 kinase alpha-6 (EC 2....)	81	7e-15
sp	Q9NWZ3	IRAK4_HUMAN Interleukin-1 receptor-associated kinase 4...	81	7e-15
sp	Q9UPZ9	ICK_HUMAN Serine/threonine-protein kinase ICK (EC 2.7....)	81	7e-15
sp	Q9P232	CNTN3_HUMAN Contactin-3 precursor (Brain-derived immun...)	81	7e-15
tr	Q69FE3	_HUMAN Interleukin-1 receptor-associated kinase 4 varia...	81	7e-15
tr	Q5JR99	_HUMAN Polo-like kinase 3 (Drosophila) [PLK3] [Homo sap...]	81	7e-15
tr	O75271	_HUMAN R31237_1, (Fragment) [Homo sapiens (Human)]	81	7e-15
tr	A7MD41	_HUMAN Intestinal cell (MAK-like) kinase (Intestinal ce...)	81	7e-15
tr	A6NKA6	_HUMAN Uncharacterized protein CDKL5 [CDKL5] [Homo sapi...]	81	7e-15
tr	A6NHD7	_HUMAN Uncharacterized protein NEK11 [NEK11] [Homo sapi...]	81	7e-15
sp_vs	Q8NG66-2	Isoform 2 of Q8NG66 - Homo sapiens (Human) [NEK11...]	81	7e-15
sp_vs	Q8NG66-3	Isoform 3 of Q8NG66 - Homo sapiens (Human) [NEK11...]	81	7e-15
sp	Q13153	PAK1_HUMAN Serine/threonine-protein kinase PAK 1 (EC 2...)	80	9e-15
sp	Q99683	M3K5_HUMAN Mitogen-activated protein kinase kinase kin...	80	9e-15
tr	Q6ZN12	_HUMAN cDNA FLJ16039 fis, clone ADRL2001554, weakly si...	80	9e-15
tr	Q59GL6	_HUMAN Mitogen-activated protein kinase kinase kinase 5...	80	9e-15
tr	A6NKM9	_HUMAN Uncharacterized protein MAP3K5 (Fragment) [MAP3K...]	80	9e-15
tr	A6NIA0	_HUMAN Uncharacterized protein MAP3K5 [MAP3K5] [Homo sa...]	80	9e-15
sp	Q9BYT3	STK33_HUMAN Serine/threonine-protein kinase 33 (EC 2.7...)	80	1e-14
sp	Q9NYY3	PLK2_HUMAN Serine/threonine-protein kinase PLK2 (EC 2....)	80	1e-14
sp	Q8IVH8	M4K3_HUMAN Mitogen-activated protein kinase kinase kin...	80	1e-14
sp	P54646	AAPK2_HUMAN 5'-AMP-activated protein kinase catalytic ...	80	1e-14
tr	Q92626	_HUMAN Peroxidasin homolog (Melanoma-associated antigen...)	80	1e-14
tr	Q8N7M6	_HUMAN cDNA FLJ40844 fis, clone TRACH2014356, highly si...	80	1e-14
tr	Q6IQ39	_HUMAN MAP4K3 protein (Mitogen-activated protein kinase...)	80	1e-14
tr	Q69FE1	_HUMAN Interleukin-1 receptor-associated kinase 4 short...	80	1e-14
tr	Q4KMG2	_HUMAN PXDN protein (Fragment) [PXDN] [Homo sapiens (Hu...]	80	1e-14

<input type="checkbox"/>	sp_vs	Q8IVH8-3	Isoform 3 of Q8IVH8 - Homo sapiens (Human) [MAP4K...	80	1e-14
<input type="checkbox"/>	sp	Q9UKE5	TNIK_HUMAN TRAF2 and NCK-interacting protein kinase (E...	80	2e-14
<input type="checkbox"/>	sp	P20794	MAK_HUMAN Serine/threonine-protein kinase MAK (EC 2.7....	80	2e-14
<input type="checkbox"/>	sp	P57058	HUNK_HUMAN Hormonally up-regulated neu tumor-associate...	80	2e-14
<input type="checkbox"/>	sp	O76039	CDKL5_HUMAN Cyclin-dependent kinase-like 5 (EC 2.7.11....	80	2e-14
<input type="checkbox"/>	sp	Q92772	CDKL2_HUMAN Cyclin-dependent kinase-like 2 (EC 2.7.11....	80	2e-14
<input type="checkbox"/>	tr	Q8IXN4	_HUMAN MAK protein [Homo sapiens (Human)]	80	2e-14
<input type="checkbox"/>	tr	Q547D0	_HUMAN Male germ cell-associated kinase (Male germ cell...	80	2e-14
<input type="checkbox"/>	tr	A7E2A3	_HUMAN TRAF2 and NCK interacting kinase (TRAF2 and NCK ...	80	2e-14
<input type="checkbox"/>	tr	A0MZT5	_HUMAN AMP-activated alpha 2 subunit [PRKAA2] [Homo sap...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-2	Isoform 2 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-3	Isoform 3 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-4	Isoform 4 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-5	Isoform 5 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-6	Isoform 6 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-7	Isoform 7 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-8	Isoform 8 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp	Q00537	PCTK2_HUMAN Serine/threonine-protein kinase PCTAIRE-2 ...	79	2e-14
<input type="checkbox"/>	sp	Q8TD19	NEK9_HUMAN Serine/threonine-protein kinase Nek9 (EC 2....	79	2e-14
<input type="checkbox"/>	sp	Q8IWV2	CNTN4_HUMAN Contactin-4 precursor (Brain-derived immun...	79	2e-14
<input type="checkbox"/>	tr	Q59FN2	_HUMAN P21-activated kinase 2 variant (Fragment) [Homo ...	79	2e-14
<input type="checkbox"/>	sp_vs	Q8IWV2-3	Isoform 3 of Q8IWV2 - Homo sapiens (Human) [CNTN4...	79	2e-14
<input type="checkbox"/>	sp	Q8IYT8	ULK2_HUMAN Serine/threonine-protein kinase ULK2 (EC 2....	79	3e-14
<input type="checkbox"/>	sp	Q8IVT5	KSR1_HUMAN Kinase suppressor of Ras 1 [KSR1] [Homo sap...	79	3e-14
<input type="checkbox"/>	sp	Q4KMG0	CDON_HUMAN Cell adhesion molecule-related/down-regulat...	79	3e-14
<input type="checkbox"/>	tr	Q8NC04	_HUMAN CDNA FLJ90626 fis, clone PLACE1003135, weakly si...	79	3e-14
<input type="checkbox"/>	tr	Q15523	_HUMAN Serine/threonine protein kinase [Homo sapiens (H...	79	3e-14
<input type="checkbox"/>	sp_vs	Q4KMG0-2	Isoform 2 of Q4KMG0 - Homo sapiens (Human) [CDON]...	79	3e-14
<input type="checkbox"/>	sp_vs	Q8IVT5-2	Isoform 2 of Q8IVT5 - Homo sapiens (Human) [KSR1]...	79	3e-14
<input type="checkbox"/>	sp_vs	Q8IVT5-3	Isoform 3 of Q8IVT5 - Homo sapiens (Human) [KSR1]...	79	3e-14
<input type="checkbox"/>	sp	Q15759	MK11_HUMAN Mitogen-activated protein kinase 11 (EC 2.7...	79	4e-14
<input type="checkbox"/>	sp	P51841	GUC2F_HUMAN Retinal guanylyl cyclase 2 precursor (EC 4...	79	4e-14
<input type="checkbox"/>	tr	Q86VU3	_HUMAN MAP4K2 protein (Mitogen-activated protein kinase...	79	4e-14
<input type="checkbox"/>	sp_vs	Q96S53-2	Isoform 2 of Q96S53 - Homo sapiens (Human) [TESK2...	79	4e-14
<input type="checkbox"/>	sp	Q8N4C8	MINK1_HUMAN Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...	78	5e-14
<input type="checkbox"/>	sp	Q92918	M4K1_HUMAN Mitogen-activated protein kinase kinase kin...	78	5e-14
<input type="checkbox"/>	sp	Q8IWV4	CDKL3_HUMAN Cyclin-dependent kinase-like 3 (EC 2.7.11....	78	5e-14
<input type="checkbox"/>	tr	Q5U8Z0	_HUMAN Misshapen/NIKs-related kinase isoform beta [MINK...]	78	5e-14
<input type="checkbox"/>	tr	Q5JPK7	_HUMAN Ribosomal protein S6 kinase, 90kDa, polypeptide ...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8IWV4-2	Isoform 2 of Q8IWV4 - Homo sapiens (Human) [CDKL3...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8IVH8-2	Isoform 2 of Q8IVH8 - Homo sapiens (Human) [MAP4K...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8N4C8-2	Isoform 1 of Q8N4C8 - Homo sapiens (Human) [MINK1...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8N4C8-3	Isoform 2 of Q8N4C8 - Homo sapiens (Human) [MINK1...	78	5e-14
<input type="checkbox"/>	sp_vs	Q59H18-4	Isoform 4 of Q59H18 - Homo sapiens (Human) [TNNI3...	78	5e-14
<input type="checkbox"/>	sp	O75914	PAK3_HUMAN Serine/threonine-protein kinase PAK 3 (EC 2...	78	6e-14
<input type="checkbox"/>	sp	O95819	M4K4_HUMAN Mitogen-activated protein kinase kinase kin...	78	6e-14
<input type="checkbox"/>	tr	Q6ZMM4	_HUMAN CDNA FLJ16821 fis, clone TRACH3021066, highly si...	78	6e-14
<input type="checkbox"/>	tr	Q59ED6	_HUMAN Polo-like kinase 3 variant (Fragment) [Homo sapi...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-2	Isoform 2 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-3	Isoform 3 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-4	Isoform 4 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-5	Isoform 5 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O75914-2	Isoform 2 of O75914 - Homo sapiens (Human) [PAK3]...	78	6e-14
<input type="checkbox"/>	sp	O75385	ULK1_HUMAN Serine/threonine-protein kinase ULK1 (EC 2....	77	8e-14
<input type="checkbox"/>	sp	Q96PF2	TSSK2_HUMAN Testis-specific serine/threonine-protein k...	77	8e-14
<input type="checkbox"/>	sp	Q7L7X3	TAOK1_HUMAN Serine/threonine-protein kinase TAO1 (EC 2...	77	8e-14
<input type="checkbox"/>	sp	Q12851	M4K2_HUMAN Mitogen-activated protein kinase kinase kin...	77	8e-14
<input type="checkbox"/>	sp	P05129	KPCG_HUMAN Protein kinase C gamma type (EC 2.7.11.13) ...	77	8e-14
<input type="checkbox"/>	tr	Q6A1A2	_HUMAN PDPK2 protein [PDPK2] [Homo sapiens (Human)]	77	8e-14
<input type="checkbox"/>	tr	A2RUT8	_HUMAN TAO kinase 1 (TAO kinase 1, isoform CRA_a) [TAOK...	77	8e-14
<input type="checkbox"/>	tr	A0ZT99	_HUMAN Testis-specific serine kinase 2 (HCG1641087) [TS...	77	8e-14
<input type="checkbox"/>	sp	P53350	PLK1_HUMAN Serine/threonine-protein kinase PLK1 (EC 2....	77	1e-13
<input type="checkbox"/>	sp	Q14012	KCC1A_HUMAN Calcium/calmodulin-dependent protein kinas...	77	1e-13
<input type="checkbox"/>	sp_vs	Q96RW7-3	Isoform 3 of Q96RW7 - Homo sapiens (Human) [HMCN1...	77	1e-13
<input type="checkbox"/>	sp	Q6PHR2	ULK3_HUMAN Serine/threonine-protein kinase ULK3 (EC 2....	77	1e-13
<input type="checkbox"/>	sp	O15530	PDPK1_HUMAN 3-phosphoinositide-dependent protein kinas...	77	1e-13

<input type="checkbox"/>	sp	Q00536	PCTK1_HUMAN Serine/threonine-protein kinase PCTAIRE-1 ...	77	1e-13
<input type="checkbox"/>	sp	Q16539	MK14_HUMAN Mitogen-activated protein kinase 14 (EC 2.7...)	77	1e-13
<input type="checkbox"/>	tr	Q9UPJ8	_HUMAN PkB-like (Fragment) [PkB-like 1] [Homo sapiens (...]	77	1e-13
<input type="checkbox"/>	tr	Q9BRL4	_HUMAN PCTK1 protein [PCTK1] [Homo sapiens (Human)]	77	1e-13
<input type="checkbox"/>	tr	Q96GA5	_HUMAN PCTK1 protein (Fragment) [PCTK1] [Homo sapiens (...]	77	1e-13
<input type="checkbox"/>	tr	Q6FI20	_HUMAN PDPK1 protein [PDPK1] [Homo sapiens (Human)]	77	1e-13
<input type="checkbox"/>	tr	Q59EH6	_HUMAN 3-phosphoinositide dependent protein kinase-1 va...	77	1e-13
<input type="checkbox"/>	tr	A6P3A7	_HUMAN Maternal embryonic leucine zipper kinase v2 [MEL...	77	1e-13
<input type="checkbox"/>	sp_vs	P11362-15	Isoform 16 of P11362 - Homo sapiens (Human) [FGF...	77	1e-13
<input type="checkbox"/>	sp_vs	Q16539-3	Isoform Mxi2 of Q16539 - Homo sapiens (Human) [MA...]	77	1e-13
<input type="checkbox"/>	sp_vs	Q16539-4	Isoform Exip of Q16539 - Homo sapiens (Human) [MA...]	77	1e-13
<input type="checkbox"/>	sp_vs	O15530-2	Isoform 2 of O15530 - Homo sapiens (Human) [PDPK1...]	77	1e-13
<input type="checkbox"/>	sp	Q9HCK4	ROBO2_HUMAN Roundabout homolog 2 precursor [ROBO2] [Ho...	76	2e-13
<input type="checkbox"/>	sp	Q9UQ07	MOK_HUMAN MAPK/MAK/MRK overlapping kinase (EC 2.7.11.2...)	76	2e-13
<input type="checkbox"/>	sp	Q5S007	LRRK2_HUMAN Leucine-rich repeat serine/threonine-prote...	76	2e-13
<input type="checkbox"/>	tr	Q19AB5	_HUMAN ROBO2 isoform a [Homo sapiens (Human)]	76	2e-13
<input type="checkbox"/>	tr	Q19AB4	_HUMAN ROBO2 isoform b (Roundabout, axon guidance recep...	76	2e-13
<input type="checkbox"/>	tr	Q17RV3	_HUMAN Leucine-rich repeat kinase 2 [LRRK2] [Homo sapie...	76	2e-13
<input type="checkbox"/>	tr	A6NJU2	_HUMAN Uncharacterized protein LRRK2 [LRRK2] [Homo sapi...	76	2e-13
<input type="checkbox"/>	tr	A6NC64	_HUMAN Uncharacterized protein SNF1LK [SNF1LK] [Homo sa...	76	2e-13
<input type="checkbox"/>	sp_vs	Q9UQ07-2	Isoform 2 of Q9UQ07 - Homo sapiens (Human) [RAGE]...	76	2e-13
<input type="checkbox"/>	sp_vs	Q9HCK4-2	Isoform 2 of Q9HCK4 - Homo sapiens (Human) [ROBO2...]	76	2e-13
<input type="checkbox"/>	sp	Q8WZ42	TITIN_HUMAN Titin (EC 2.7.11.1) (Connectin) (Rhabdomyo...	76	2e-13
<input type="checkbox"/>	sp	Q9Y2K2	QSK_HUMAN Serine/threonine-protein kinase QSK (EC 2.7....)	76	2e-13
<input type="checkbox"/>	sp	Q00535	CDK5_HUMAN Cell division protein kinase 5 (EC 2.7.11.2...)	76	2e-13
<input type="checkbox"/>	tr	Q9NWX4	_HUMAN CDNA FLJ20549 fis, clone KAT11561 [Homo sapiens ...]	76	2e-13
<input type="checkbox"/>	tr	A6NTI10	_HUMAN Uncharacterized protein ENSP00000364441 [Homo sa...	76	2e-13
<input type="checkbox"/>	tr	A1A5A8	_HUMAN KIAA0999 protein [KIAA0999] [Homo sapiens (Human)]	76	2e-13
<input type="checkbox"/>	sp_vs	Q9Y2K2-3	Isoform 3 of Q9Y2K2 - Homo sapiens (Human) [QSK] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-2	Isoform 2 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-4	Isoform 4 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-5	Isoform 5 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-7	Isoform 7 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-8	Isoform 8 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp	Q9NQU5	PAK6_HUMAN Serine/threonine-protein kinase PAK 6 (EC 2...	75	3e-13
<input type="checkbox"/>	sp	Q7Z2Y5	NRK_HUMAN Nik-related protein kinase (EC 2.7.11.1) [NR...	75	3e-13
<input type="checkbox"/>	sp	Q6VAB6	KSR2_HUMAN Kinase suppressor of Ras 2 (hKSR2) [KSR2] [...]	75	3e-13
<input type="checkbox"/>	sp	P24941	CDK2_HUMAN Cell division protein kinase 2 (EC 2.7.11.2...)	75	3e-13
<input type="checkbox"/>	tr	Q59GT1	_HUMAN Conserved helix-loop-helix ubiquitous kinase var...	75	3e-13
<input type="checkbox"/>	tr	Q53HJ9	_HUMAN 3-phosphoinositide dependent protein kinase-1 va...	75	3e-13
<input type="checkbox"/>	tr	A7E2B2	_HUMAN CRKRS protein [CRKRS] [Homo sapiens (Human)]	75	3e-13
<input type="checkbox"/>	sp	Q9P286	PAK7_HUMAN Serine/threonine-protein kinase PAK 7 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	Q8IY84	NIM1_HUMAN Serine/threonine-protein kinase NIM1 (EC 2....)	75	4e-13
<input type="checkbox"/>	sp	P51955	NEK2_HUMAN Serine/threonine-protein kinase Nek2 (EC 2....)	75	4e-13
<input type="checkbox"/>	sp	O15111	IKKA_HUMAN Inhibitor of nuclear factor kappa-B kinase ...	75	4e-13
<input type="checkbox"/>	sp	P11802	CDK4_HUMAN Cell division protein kinase 4 (EC 2.7.11.2...)	75	4e-13
<input type="checkbox"/>	sp	Q9NYV4	CD2L7_HUMAN Cell division cycle 2-related protein kina...	75	4e-13
<input type="checkbox"/>	sp	Q14004	CD2L5_HUMAN Cell division cycle 2-like protein kinase ...	75	4e-13
<input type="checkbox"/>	tr	Q9BVE2	_HUMAN CDC2L5 protein [Homo sapiens (Human)]	75	4e-13
<input type="checkbox"/>	tr	Q8TB93	_HUMAN P21(CDKN1A)-activated kinase 7 [PAK7] [Homo sapi...	75	4e-13
<input type="checkbox"/>	tr	Q6FG61	_HUMAN CDK4 protein (Cyclin-dependent kinase 4, isoform...	75	4e-13
<input type="checkbox"/>	tr	Q562E6	_HUMAN Conserved helix-loop-helix ubiquitous kinase [CH...	75	4e-13
<input type="checkbox"/>	sp_vs	Q14004-2	Isoform 2 of Q14004 - Homo sapiens (Human) [CDC2L...	75	4e-13
<input type="checkbox"/>	sp_vs	Q16539-2	Isoform CSBP1 of Q16539 - Homo sapiens (Human) [M...	75	4e-13
<input type="checkbox"/>	sp_vs	P51955-2	Isoform 2 of P51955 - Homo sapiens (Human) [NEK2]...	75	4e-13
<input type="checkbox"/>	sp_vs	P51955-3	Isoform 3 of P51955 - Homo sapiens (Human) [NEK2]...	75	4e-13
<input type="checkbox"/>	sp	Q9H2K8	TAOK3_HUMAN Serine/threonine-protein kinase TAO3 (EC 2...	75	5e-13
<input type="checkbox"/>	sp	Q9UEE5	ST17A_HUMAN Serine/threonine-protein kinase 17A (EC 2....)	75	5e-13
<input type="checkbox"/>	sp	Q07002	PCTK3_HUMAN Serine/threonine-protein kinase PCTAIRE-3 ...	75	5e-13
<input type="checkbox"/>	sp	Q9NZJ5	E2AK3_HUMAN Eukaryotic translation initiation factor 2...	75	5e-13
<input type="checkbox"/>	tr	Q6V3A3	_HUMAN PCTAIRE protein kinase 3 isoform a (PCTAIRE prot...	75	5e-13
<input type="checkbox"/>	tr	Q6V3A2	_HUMAN PCTAIRE protein kinase 3 isoform b (PCTAIRE prot...	75	5e-13
<input type="checkbox"/>	tr	Q6IAW3	_HUMAN CDK5 protein [CDK5] [Homo sapiens (Human)]	75	5e-13
<input type="checkbox"/>	tr	Q68DI6	_HUMAN Putative uncharacterized protein DKFZp781H1925 [...]	75	5e-13
<input type="checkbox"/>	tr	Q59G02	_HUMAN PCTAIRE protein kinase 3 isoform b variant (Frag...	75	5e-13
<input type="checkbox"/>	tr	Q53QY0	_HUMAN Putative uncharacterized protein EIF2AK3 (Fragme...	75	5e-13

[checkbox]	tr	A4D1V6	_HUMAN Serine/threonine kinase 17a (Apoptosis-inducing)...	75	5e-13
[checkbox]	tr	A0AVH1	_HUMAN Eukaryotic translation initiation factor 2-alpha...	75	5e-13
[checkbox]	sp	Q8NEV4	MYO3A_HUMAN Myosin IIIA (EC 2.7.11.1) [MYO3A] [Homo sa...	74	7e-13
[checkbox]	sp	Q9UQ52	CNTN6_HUMAN Contactin-6 precursor (Neural recognition ...	74	7e-13
[checkbox]	tr	Q9Y6B5	_HUMAN PAK2 [Homo sapiens (Human)]	74	7e-13
[checkbox]	tr	Q6ZWT8	_HUMAN CDNA FLJ14395 fis, clone HEMBA1003250, weakly si...	74	7e-13
[checkbox]	tr	Q5VX13	_HUMAN Myosin IIIA [MYO3A] [Homo sapiens (Human)]	74	7e-13
[checkbox]	tr	Q0VD65	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	74	7e-13
[checkbox]	tr	Q05AG9	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	74	7e-13
[checkbox]	sp	Q15831	STK11_HUMAN Serine/threonine-protein kinase 11 (EC 2.7...	74	9e-13
[checkbox]	sp	Q00444	PLK4_HUMAN Serine/threonine-protein kinase PLK4 (EC 2....	74	9e-13
[checkbox]	sp	P23443	KS6B1_HUMAN Ribosomal protein S6 kinase beta-1 (EC 2.7...	74	9e-13
[checkbox]	tr	Q9HSS3	_HUMAN Putative uncharacterized protein [Homo sapiens (...	74	9e-13
[checkbox]	tr	Q7Z721	_HUMAN RPS6KB1 protein (Ribosomal protein S6 kinase, 70...	74	9e-13
[checkbox]	sp_vs	P23443-2	Isoform Alpha II of P23443 - Homo sapiens (Human)...	74	9e-13
[checkbox]	sp	O94856	NFASC_HUMAN Neurofascin precursor [NFASC] [Homo sapien...	74	1e-12
[checkbox]	tr	Q9H4D1	_HUMAN Protein kinase [dik] [Homo sapiens (Human)]	74	1e-12
[checkbox]	tr	Q2TB16	_HUMAN Receptor-interacting serine-threonine kinase 4 (...	74	1e-12
[checkbox]	tr	Q15879	_HUMAN Protein kinase (Fragment) [Homo sapiens (Human)]	74	1e-12
[checkbox]	tr	Q149P5	_HUMAN NFASC protein [NFASC] [Homo sapiens (Human)]	74	1e-12
[checkbox]	sp_vs	O94856-2	Isoform 2 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-3	Isoform 3 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-4	Isoform 4 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-5	Isoform 5 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-6	Isoform 6 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-7	Isoform 7 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-8	Isoform 8 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-9	Isoform 9 of O94856 - Homo sapiens (Human) [NFASC...]	74	1e-12
[checkbox]	sp_vs	O94856-10	Isoform 10 of O94856 - Homo sapiens (Human) [NFA...]	74	1e-12
[checkbox]	sp_vs	O94856-11	Isoform 11 of O94856 - Homo sapiens (Human) [NFA...]	74	1e-12
[checkbox]	sp_vs	O94856-12	Isoform 12 of O94856 - Homo sapiens (Human) [NFA...]	74	1e-12
[checkbox]	sp_vs	O94856-13	Isoform 13 of O94856 - Homo sapiens (Human) [NFA...]	74	1e-12
[checkbox]	sp_vs	P57078-2	Isoform 2 of P57078 - Homo sapiens (Human) [RIPK4...]	74	1e-12
[checkbox]	sp	O95382	M3K6_HUMAN Mitogen-activated protein kinase kinase kin...	73	1e-12
[checkbox]	tr	Q5TI62	_HUMAN Ribosomal protein S6 kinase, 90kDa, polypeptide ...	73	1e-12
[checkbox]	tr	Q5SSD4	_HUMAN Mitogen-activated protein kinase kinase kinase 6...	73	1e-12
[checkbox]	tr	Q32MQ5	_HUMAN MAP3K6 protein [MAP3K6] [Homo sapiens (Human)]	73	1e-12
[checkbox]	sp_vs	O95382-2	Isoform 2 of O95382 - Homo sapiens (Human) [MAP3K...]	73	1e-12
[checkbox]	sp_vs	O95382-3	Isoform 3 of O95382 - Homo sapiens (Human) [MAP3K...]	73	1e-12
[checkbox]	sp_vs	Q56UN5-4	Isoform 4 of Q56UN5 - Homo sapiens (Human) [YSK4]...	73	1e-12
[checkbox]	sp	Q9BXA6	TSSK6_HUMAN Testis-specific serine/threonine-protein k...	73	2e-12
[checkbox]	sp	Q5MA15	CDKL4_HUMAN Cyclin-dependent kinase-like 4 (EC 2.7.11....	73	2e-12
[checkbox]	tr	Q8NDA2	_HUMAN Hemicentrin-2 (Fragment) [DKFZp434P0216] [Homo sa...	73	2e-12
[checkbox]	tr	Q2NME9	_HUMAN Cyclin-dependent kinase-like 4 [CDKL4] [Homo sap...	73	2e-12
[checkbox]	sp	Q9Y4K4	M4K5_HUMAN Mitogen-activated protein kinase kinase kinase...	72	3e-12
[checkbox]	tr	Q5VZ10	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	72	3e-12
[checkbox]	tr	Q53GK9	_HUMAN MAPK13 protein variant (Fragment) [Homo sapiens ...	72	3e-12
[checkbox]	sp	Q15746	MYLK_HUMAN Myosin light chain kinase, smooth muscle (E...	72	3e-12
[checkbox]	sp	P11801	KPSH1_HUMAN Serine/threonine-protein kinase H1 (EC 2.7....	72	3e-12
[checkbox]	sp	Q9C098	DCLK3_HUMAN Serine/threonine-protein kinase DCLK3 (EC ...	72	3e-12
[checkbox]	sp	Q00532	CDKL1_HUMAN Cyclin-dependent kinase-like 1 (EC 2.7.11....	72	3e-12
[checkbox]	tr	Q2M3A4	_HUMAN Cyclin-dependent kinase-like 1 (CDC2-related kin...	72	3e-12
[checkbox]	sp_vs	Q15746-2	Isoform 2 of Q15746 - Homo sapiens (Human) [MYLK]...	72	3e-12
[checkbox]	sp_vs	Q15746-6	Isoform Del-1790 of Q15746 - Homo sapiens (Human)...	72	3e-12
[checkbox]	sp	Q15264	MK13_HUMAN Mitogen-activated protein kinase 13 (EC 2.7....	72	4e-12
[checkbox]	sp	Q02156	KPCE_HUMAN Protein kinase C epsilon type (EC 2.7.11.13...)	72	4e-12
[checkbox]	sp	P50750	CDK9_HUMAN Cell division protein kinase 9 (EC 2.7.11.2...)	72	4e-12
[checkbox]	tr	Q96T11	_HUMAN CDNA FLJ14518 fis, clone NT2RM1000850, weakly si...	72	4e-12
[checkbox]	tr	Q6FI46	_HUMAN MAPK13 protein (Mitogen-activated protein kinase...	72	4e-12
[checkbox]	tr	Q6FHR4	_HUMAN MAPK13 protein (Fragment) [MAPK13] [Homo sapiens...]	72	4e-12
[checkbox]	tr	A6YR18	_HUMAN Polarization-related protein LKB1 [Homo sapiens ...]	72	4e-12
[checkbox]	sp_vs	P50750-2	Isoform 2 of P50750 - Homo sapiens (Human) [CDK9]...	72	4e-12
[checkbox]	sp	Q92823	NRCAM_HUMAN Neuronal cell adhesion molecule precursor ...	71	6e-12
[checkbox]	sp	Q8WXR4	MYO3B_HUMAN Myosin-IIIB (EC 2.7.11.1) [MYO3B] [Homo sa...	71	6e-12
[checkbox]	sp	Q8NFD2	ANKK1_HUMAN Ankyrin repeat and protein kinase domain-c...	71	6e-12
[checkbox]	tr	Q59F15	_HUMAN Protein kinase C, alpha variant (Fragment) [Homo...	71	6e-12

tr	Q4KMQ7	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
tr	Q14CA1	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
tr	Q14BM2	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
tr	A4D0S3	_HUMAN Neuronal cell adhesion molecule (Neuronal cell adhesion molecule) [Homo sapiens (Human)]	71	6e-12
sp_vs	Q8WXR4-2	Isoform 2 of Q8WXR4 - Homo sapiens (Human) [MYO3B...]	71	6e-12
sp_vs	Q8WXR4-3	Isoform 3 of Q8WXR4 - Homo sapiens (Human) [MYO3B...]	71	6e-12
sp_vs	Q8WXR4-4	Isoform 4 of Q8WXR4 - Homo sapiens (Human) [MYO3B...]	71	6e-12
sp_vs	Q8WXR4-5	Isoform 5 of Q8WXR4 - Homo sapiens (Human) [MYO3B...]	71	6e-12
sp_vs	Q8WXR4-6	Isoform 6 of Q8WXR4 - Homo sapiens (Human) [MYO3B...]	71	6e-12
sp_vs	Q8WXR4-7	Isoform 7 of Q8WXR4 - Homo sapiens (Human) [MYO3B...]	71	6e-12
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sp_vs	Q92823-4	Isoform 4 of Q92823 - Homo sapiens (Human) [NRCAM...]	71	6e-12
sp_vs	Q92823-5	Isoform 5 of Q92823 - Homo sapiens (Human) [NRCAM...]	71	6e-12
sp	Q9UL54	TAOK2_HUMAN Serine/threonine-protein kinase TA02 (EC 2.7.11.1)	71	7e-12
sp	Q99759	M3K3_HUMAN Mitogen-activated protein kinase kinase kinase 3	71	7e-12
tr	Q96HN9	_HUMAN Putative uncharacterized protein (Fragment) [Homologous to: Human]	71	7e-12
tr	Q8N3I9	_HUMAN Putative uncharacterized protein DKFZp762P223 (M...)	71	7e-12
tr	Q86V37	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (Human)]	71	7e-12
tr	Q6PIN8	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (Human)]	71	7e-12
tr	Q1PBM3	_HUMAN Mitogen-activated protein kinase kinase kinase 3	71	7e-12
tr	A7MCZ2	_HUMAN TAO kinase 2 (TAO kinase 2, isoform CRA_b) [TAOK2]	71	7e-12
tr	A0PJ48	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (Human)]	71	7e-12
sp_vs	Q9UL54-2	Isoform 2 of Q9UL54 - Homo sapiens (Human) [TAOK2...]	71	7e-12
sp	QGSA08	TSSK4_HUMAN Testis-specific serine/threonine-protein kinase	70	1e-11
sp	Q7Z5N4	SDK1_HUMAN Protein sidekick-1 precursor [SDK1] [Homo sapiens (Human)]	70	1e-11
sp	Q5VST9	OBSCN_HUMAN Obscurin (EC 2.7.11.1) (Obscurin-myosin light chain kinase)	70	1e-11
tr	Q6LD09	_HUMAN Tyrosine kinase (Fragment) [Homo sapiens (Human)]	70	1e-11
tr	Q5VXII1	_HUMAN Myosin IIIA (MYO3A protein) [MYO3A] [Homo sapiens (Human)]	70	1e-11
tr	A2A391	_HUMAN Obscurin, cytoskeletal calmodulin and titin-interacting protein	70	1e-11
sp_vs	Q5VST9-2	Isoform 2 of Q5VST9 - Homo sapiens (Human) [OBSCN...]	70	1e-11
sp_vs	Q5VST9-3	Isoform 3 of Q5VST9 - Homo sapiens (Human) [OBSCN...]	70	1e-11
sp_vs	Q5VST9-6	Isoform 6 of Q5VST9 - Homo sapiens (Human) [OBSCN...]	70	1e-11
sp_vs	Q7Z5N4-3	Isoform 3 of Q7Z5N4 - Homo sapiens (Human) [SDK1...]	70	1e-11
sp	Q9BXA7	TSSK1_HUMAN Testis-specific serine/threonine-protein kinase	70	1e-11
sp	Q9NRH2	SNRK_HUMAN SNF-related serine/threonine-protein kinase	70	1e-11
sp	P57078	RIPK4_HUMAN Receptor-interacting serine/threonine-protein kinase	70	1e-11
sp	Q02246	CNTN2_HUMAN Contactin-2 precursor (Axonin-1) (Axonal gap junction protein)	70	1e-11
tr	Q8NCE6	_HUMAN cDNA FLJ90299 fis, clone NT2RP2000514, highly similar to CNTN2	70	1e-11
tr	Q59FA7	_HUMAN Serine/threonine protein kinase 11 variant (Fragment)	70	1e-11
tr	Q53TX8	_HUMAN Putative uncharacterized protein MAP4K4 (Fragment)	70	1e-11
tr	A1L3A3	_HUMAN Contactin 2 (Axonal) [CNTN2] [Homo sapiens (Human)]	70	1e-11
tr	A0ZT98	_HUMAN Testis-specific serine kinase 1 [TSSK1] [Homo sapiens (Human)]	70	1e-11
sp	O96013	PAK4_HUMAN Serine/threonine-protein kinase PAK 4 (EC 2.7.11.1)	70	2e-11
sp	P13592	NCA12_HUMAN Neural cell adhesion molecule 1, 120 kDa isoform	70	2e-11
sp	P13591	NCA11_HUMAN Neural cell adhesion molecule 1, 140 kDa isoform	70	2e-11
sp	Q9NR99	MXRAS5_HUMAN Matrix-remodeling-associated protein 5 preproprotein	70	2e-11
tr	Q59PL7	_HUMAN Neural cell adhesion molecule 1, 120 kDa isoform...	70	2e-11
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sp_vs	O96013-3	Isoform 3 of O96013 - Homo sapiens (Human) [PAK4...]	70	2e-11
sp_vs	O96013-4	Isoform 4 of O96013 - Homo sapiens (Human) [PAK4...]	70	2e-11
sp_vs	Q9NRH2-2	Isoform 2 of Q9NRH2 - Homo sapiens (Human) [SNRK...]	70	2e-11
sp	Q96MS0	ROBO3_HUMAN Roundabout homolog 3 precursor (Roundabout gap junction protein)	69	2e-11
tr	Q68DA2	_HUMAN Putative uncharacterized protein DKFZp781D102 [DKFZp781D102]	69	2e-11
tr	Q59GDO	_HUMAN Polo-like kinase variant (Fragment) [Homo sapiens (Human)]	69	2e-11
tr	Q3KPG9	_HUMAN V-mos Moloney murine sarcoma viral oncogene homolog	69	2e-11
sp_vs	Q8WX93-2	Isoform 2 of Q8WX93 - Homo sapiens (Human) [PALLD...]	69	2e-11
sp_vs	Q96MS0-2	Isoform 2 of Q96MS0 - Homo sapiens (Human) [ROBO3...]	69	2e-11
sp	Q8WX93	PALLD_HUMAN Palladin (Sarcoma antigen NY-SAR-77) (SIH0...)	69	3e-11
sp	P45985	MP2K4_HUMAN Dual specificity mitogen-activated protein kinase	69	3e-11
sp	P00540	MOS_HUMAN Proto-oncogene serine/threonine-protein kinase	69	3e-11
sp	Q8IU85	KCC1D_HUMAN Calcium/calmodulin-dependent protein kinase	69	3e-11
sp	O43293	DAPK3_HUMAN Death-associated protein kinase 3 (EC 2.7.11.1)	69	3e-11
sp	Q9Y243	AKT3_HUMAN RAC-gamma serine/threonine-protein kinase (Fragment)	69	3e-11
tr	Q9BWF9	_HUMAN PCTK3 protein (Fragment) [PCTK3] [Homo sapiens (Human)]	69	3e-11

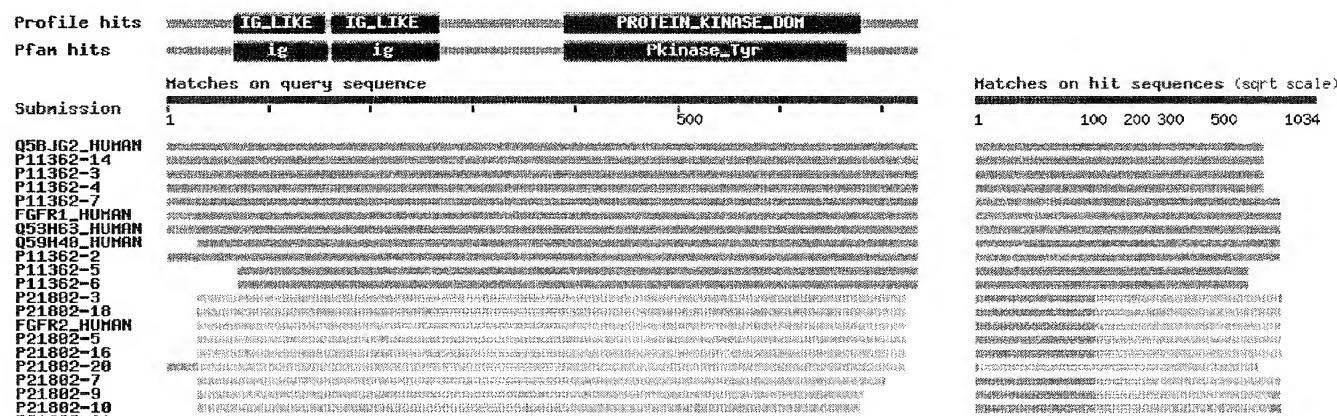
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□	tr	Q6PIE6	_HUMAN Mitogen-activated protein kinase kinase 4 [MAP2K... 69 3e-11
□	tr	Q6FHX4	_HUMAN MAP2K4 protein [MAP2K4] [Homo sapiens (Human)] 69 3e-11
□	tr	Q5VTI2	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P... 69 3e-11
□	tr	Q5VTI1	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P... 69 3e-11
□	tr	Q5SQQ7	_HUMAN Calcium/calmodulin-dependent protein kinase ID (... 69 3e-11
□	tr	Q56A86	_HUMAN AKT3 protein (Fragment) [AKT3] [Homo sapiens (Hu... 69 3e-11
□	tr	A1A4C4	_HUMAN Mitogen-activated protein kinase 4 [MAPK4] [Homo... 69 3e-11
□	sp_vs	Q9Y243-2	Isoform 2 of Q9Y243 - Homo sapiens (Human) [AKT3]... 69 3e-11
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□	sp_vs	Q8WX93-4	Isoform 4 of Q8WX93 - Homo sapiens (Human) [PALLD... 69 3e-11
□	sp_vs	Q8WX93-5	Isoform 5 of Q8WX93 - Homo sapiens (Human) [PALLD... 69 3e-11
□	sp	O00141	SGK1_HUMAN Serine/threonine-protein kinase Sgk1 (EC 2.... 69 4e-11
□	sp	P53778	MK12_HUMAN Mitogen-activated protein kinase 12 (EC 2.7.... 69 4e-11
□	sp	P31152	MK04_HUMAN Mitogen-activated protein kinase 4 (EC 2.7.... 69 4e-11
□	sp	Q9Y2U5	M3K2_HUMAN Mitogen-activated protein kinase kinase kin... 69 4e-11
□	sp	Q96RR4	KKCC2_HUMAN Calcium/calmodulin-dependent protein kinas... 69 4e-11
□	sp	Q8IWQ3	BRSK2_HUMAN BR serine/threonine-protein kinase 2 (EC 2... 69 4e-11
□	tr	Q6LC83	_HUMAN Cyclin dependent protein kinase (Cyclin-dependen... 69 4e-11
□	tr	Q5VY65	_HUMAN Serum/glucocorticoid regulated kinase [SGK] [Hom... 69 4e-11
□	tr	Q5TCN4	_HUMAN Serum/glucocorticoid regulated kinase [SGK] [Hom... 69 4e-11
□	tr	Q5TCN2	_HUMAN Serum/glucocorticoid regulated kinase (Serum/glu... 69 4e-11
□	tr	Q0VG04	_HUMAN Mitogen-activated protein kinase 4 (Mitogen-acti... 69 4e-11
□	tr	A5PKY1	_HUMAN TAO kinase 2 [TAOK2] [Homo sapiens (Human)] 69 4e-11
□	sp_vs	Q8TDC3-2	Isoform 2 of Q8TDC3 - Homo sapiens (Human) [BRSK1... 69 4e-11
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□	sp_vs	Q8IWQ3-4	Isoform 4 of Q8IWQ3 - Homo sapiens (Human) [BRSK2... 69 4e-11
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□	sp_vs	Q8WX93-7	Isoform 7 of Q8WX93 - Homo sapiens (Human) [PALLD... 69 4e-11
□	sp	Q96NX5	KCC1G_HUMAN Calcium/calmodulin-dependent protein kinas... 68 5e-11
□	sp	Q8TDC3	BRSK1_HUMAN BR serine/threonine-protein kinase 1 (EC 2... 68 5e-11
□	tr	Q86VY5	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)] 68 5e-11
□	tr	Q69YJ3	_HUMAN Putative uncharacterized protein DKFZp762L185 (F... 68 5e-11
□	tr	Q15457	_HUMAN Protein-tyrosine kinase (Fragment) [Homo sapiens... 68 5e-11
□	tr	A2A344	_HUMAN ADAMTS-like 1 [ADAMTSL1] [Homo sapiens (Human)] 68 5e-11
□	sp_vs	Q96NX5-2	Isoform 2 of Q96NX5 - Homo sapiens (Human) [CAMK1... 68 5e-11
□	sp_vs	Q15746-3	Isoform 3A of Q15746 - Homo sapiens (Human) [MYLK... 68 5e-11
□	sp_vs	Q15746-4	Isoform 3B of Q15746 - Homo sapiens (Human) [MYLK... 68 5e-11
□	sp	Q9UBEB8	NLK_HUMAN Serine/threonine kinase NLK (EC 2.7.11.24) (... 68 6e-11
□	sp	Q9H1R3	MYLK2_HUMAN Myosin light chain kinase 2, skeletal/card... 68 6e-11
□	sp	Q96JAI1	LRIG1_HUMAN Leucine-rich repeats and immunoglobulin-li... 68 6e-11
□	sp	Q96QS6	KPSH2_HUMAN Serine/threonine-protein kinase H2 (EC 2.7... 68 6e-11
□	sp	P14619	KGP1B_HUMAN cGMP-dependent protein kinase 1, beta isoz... 68 6e-11
□	sp	Q13976	KGP1A_HUMAN cGMP-dependent protein kinase 1, alpha iso... 68 6e-11
□	sp	P19525	E2AK2_HUMAN Interferon-induced, double-stranded RNA-ac... 68 6e-11
□	tr	Q9BXC3	_HUMAN Serine/threonine protein kinase MST4a (Mst3 and ... 68 6e-11
□	tr	Q8IW76	_HUMAN EIF2AK2 protein (Fragment) [EIF2AK2] [Homo sapie... 68 6e-11
□	tr	Q7Z6F6	_HUMAN Interferon-inducible double-stranded RNA-depend... 68 6e-11
□	tr	Q6E0B2	_HUMAN Small intestine SPAK-like kinase [Homo sapiens (... 68 6e-11
□	tr	Q5XWD3	_HUMAN Leucine-rich repeat protein LRIG1 [LRIG1] [Homo ... 68 6e-11
□	tr	Q5SQU3	_HUMAN Protein kinase, cGMP-dependent, type I [PRKG1] [... 68 6e-11
□	sp_vs	P11362-17	Isoform 3 of P11362 - Homo sapiens (Human) [FGFR... 68 6e-11
□	sp	P27173	TGFR2_HUMAN TGF-beta receptor type-2 precursor (EC 2.7... 67 8e-11
□	sp	Q9UBF9	MYOT1_HUMAN Myotilin (Titin immunoglobulin domain prot... 67 8e-11
□	sp	Q13163	MP2K5_HUMAN Dual specificity mitogen-activated protein... 67 8e-11
□	sp	P53355	DAPK1_HUMAN Death-associated protein kinase 1 (EC 2.7.... 67 8e-11
□	sp	Q12860	CNTN1_HUMAN Contactin-1 precursor (Neural cell surface... 67 8e-11
□	sp	Q9UQ88	CD2L2_HUMAN PITSLRE serine/threonine-protein kinase CD... 67 8e-11

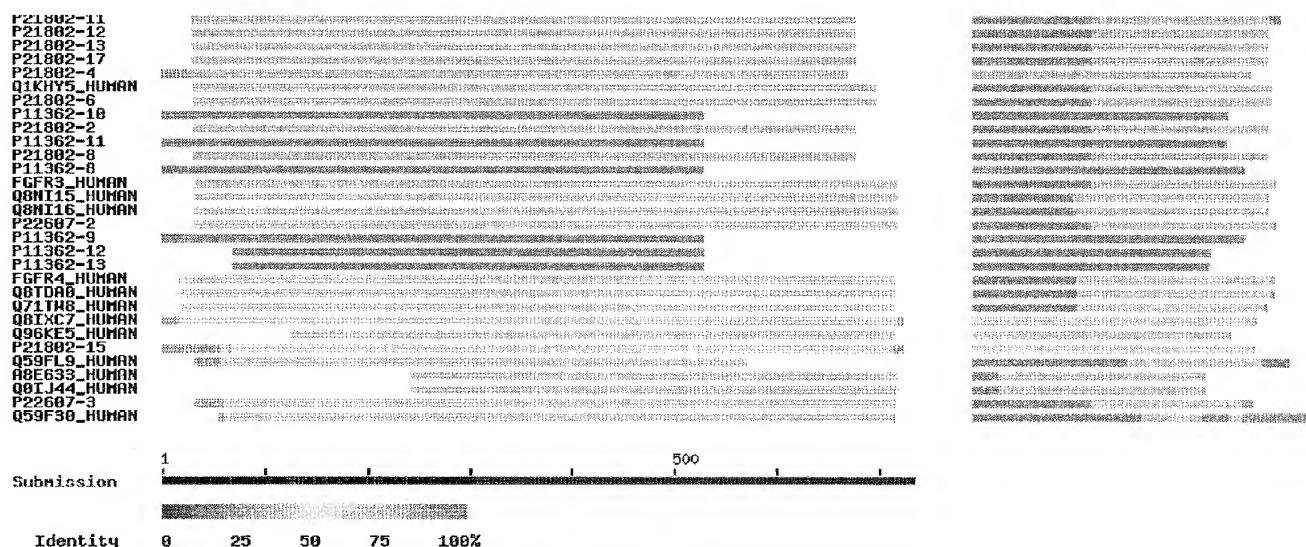
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<input type="checkbox"/>	sp	P31751	AKT2_HUMAN RAC-beta serine/threonine-protein kinase (E...	66	2e-10
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<input type="checkbox"/>	sp_vs	P21127-4	Isoform 3 of P21127 - Homo sapiens (Human) [CDC2L...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-5	Isoform SV4 of P21127 - Homo sapiens (Human) [CDC...	66	2e-10

sp_vs	P21127-6	Isoform SV5 of P21127 - Homo sapiens (Human) [CDC...	66	2e-10
sp_vs	P21127-8	Isoform 8 of P21127 - Homo sapiens (Human) [CDC2L...	66	2e-10
sp_vs	P21127-9	Isoform SV10 of P21127 - Homo sapiens (Human) [CD...	66	2e-10
sp_vs	P21127-10	Isoform SV11 of P21127 - Homo sapiens (Human) [C...	66	2e-10
sp_vs	P21127-12	Isoform 7 of P21127 - Homo sapiens (Human) [CDC2...	66	2e-10
sp_vs	Q96RG2-2	Isoform 2 of Q96RG2 - Homo sapiens (Human) [PASK]...	66	2e-10
sp_vs	O15530-3	Isoform 3 of O15530 - Homo sapiens (Human) [PDPK1...	66	2e-10
sp	O43930	PRKY_HUMAN Serine/threonine-protein kinase PRKY (EC 2....	65	3e-10
sp	P98160	PGEM_HUMAN Basement membrane-specific heparan sulfate ...	65	3e-10
sp	Q38SD2	LRRK1_HUMAN Leucine-rich repeat serine/threonine-prote...	65	3e-10
sp	P24723	KPCL_HUMAN Protein kinase C eta type (EC 2.7.11.13) (n...	65	3e-10
sp	Q8N5S9	KKCC1_HUMAN Calcium/calmodulin-dependent protein kinas...	65	3e-10
sp	Q04771	ACVR1_HUMAN Activin receptor type-I precursor (EC 2.7....	65	3e-10
tr	Q8NE03	_HUMAN Protein kinase C, eta (Protein kinase C, eta, is...	65	3e-10
tr	Q5VU27	_HUMAN Heparan sulfate proteoglycan 2 [HSPG2] [Homo sap...	65	3e-10
tr	A8CZ58	_HUMAN Extracellular signal-regulated kinase-1 splice v...	65	3e-10
tr	A6NDF7	_HUMAN Uncharacterized protein HSPG2 [HSPG2] [Homo sapi...	65	3e-10
tr	A6H8V9	_HUMAN LRRK1 protein (Fragment) [LRRK1] [Homo sapiens (...	65	3e-10
sp_vs	Q38SD2-3	Isoform 3 of Q38SD2 - Homo sapiens (Human) [LRRK1...	65	3e-10
sp	O94768	ST17B_HUMAN Serine/threonine-protein kinase 17B (EC 2....	65	4e-10
sp	O14976	GAK_HUMAN Cyclin G-associated kinase (EC 2.7.11.1) [GA...	65	4e-10
tr	Q6FG98	_HUMAN STK17B protein [STK17B] [Homo sapiens (Human)]	65	4e-10
tr	Q53QB7	_HUMAN Putative uncharacterized protein STK17B (Serine/...	65	4e-10
sp_vs	Q8TD08-2	Isoform 2 of Q8TD08 - Homo sapiens (Human) [MAPK1...	65	4e-10
sp	Q496M5	PLK5_HUMAN Serine/threonine-protein kinase PLK5 (EC 2....	65	5e-10
sp	Q92859	NEO1_HUMAN Neogenin precursor [NEO1] [Homo sapiens (Hu...	65	5e-10
sp	Q6P2M8	KCC1B_HUMAN Calcium/calmodulin-dependent protein kinas...	65	5e-10
sp	O15075	DCLK1_HUMAN Serine/threonine-protein kinase DCLK1 (EC ...	65	5e-10
tr	Q5VZ21	_HUMAN Doublecortin and CaM kinase-like 1 (Doublecortin...	65	5e-10
tr	Q5VZZ0	_HUMAN Doublecortin and CaM kinase-like 1 (Doublecortin...	65	5e-10
tr	Q5VZY8	_HUMAN Doublecortin and CaM kinase-like 1 [DCAMKL1] [Ho...	65	5e-10
tr	Q3MS94	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	65	5e-10
tr	A6NI35	_HUMAN Uncharacterized protein HSPG2 [HSPG2] [Homo sapi...	65	5e-10
tr	A6NHX2	_HUMAN Uncharacterized protein ENSP00000329329 (Fragmen...	65	5e-10
sp_vs	O15075-2	Isoform 1 of O15075 - Homo sapiens (Human) [DCLK1...	65	5e-10
sp_vs	O15075-3	Isoform 3 of O15075 - Homo sapiens (Human) [DCLK1...	65	5e-10
sp_vs	O15075-4	Isoform 4 of O15075 - Homo sapiens (Human) [DCLK1...	65	5e-10
sp_vs	Q92859-2	Isoform 2 of Q92859 - Homo sapiens (Human) [NEO1]...	65	5e-10
sp_vs	Q496M5-2	Isoform 2 of Q496M5 - Homo sapiens (Human) [PLK5]...	65	5e-10
sp	Q32MK0	MYLK3_HUMAN Putative myosin light chain kinase 3 (EC 2...	64	7e-10
sp	Q13233	M3K1_HUMAN Mitogen-activated protein kinase kinase kin...	64	7e-10
sp	Q13555	KCC2G_HUMAN Calcium/calmodulin-dependent protein kinas...	64	7e-10
sp	P22612	KAPCG_HUMAN cAMP-dependent protein kinase, gamma-catal...	64	7e-10
sp	P36894	BMR1A_HUMAN Bone morphogenetic protein receptor type I...	64	7e-10
sp	P20594	ANPRB_HUMAN Atrial natriuretic peptide receptor B prec...	64	7e-10

Graphical overview of the alignments

[Click here](#) to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs
 (* Help) (use ScanProsite for more details about PROSITE matches)





Alignments

tr Q5BJG2 Fibroblast growth factor receptor 1 (Fms-related tyrosine kinase 2, 731 AA
Q5BJG2_HUMAN Pfeiffer syndrome) [FGFR1] [Homo sapiens (Human)] align

Score = 1420 bits (3677), Expect = 0.0
Identities = 696/735 (94%), Positives = 709/735 (96%), Gaps = 6/735 (0%)

Query: 1 MWGKCLLFWAVLVATLCTARPAPTLPEQDALPSSEDDDDDSSEEKETDNTKPNPV 60
MW WKCLLFWAVLVATLCTARP+PTLPEQDALPSSEDDDDDSSEEKETDNTKPNPV
Sbjct: 1 MWSWKCLLFWAVLVATLCTARPSPTLPEQDALPSSEDDDDDSSEEKETDNTKPNPV 60

Query: 61 APYWTSPKEMEKKLHAVPAAKTVKFCPSSGTNPNTLRWLKNKGKEFKPDHRIGGYKVRYA 120
APYWTSPKEMEKKLHAVPAAKTVKFCPSSGTNPNTLRWLKNKGKEFKPDHRIGGYKVRYA
Sbjct: 61 APYWTSPKEMEKKLHAVPAAKTVKFCPSSGTNPNTLRWLKNKGKEFKPDHRIGGYKVRYA 120

Query: 121 TWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGS 180
TWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGS
Sbjct: 121 TWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGS 180

Query: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILK +G+N++D E VL L NV 238
NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILK +G+N++D E VL L NV
Sbjct: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKTAGVNNTDKEMEVHLRNV 240

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFLI 298
+GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAFLI
Sbjct: 241 SFEDAGEYTCLAGNSIGLSHHSATLTVL---EALEERPAVMTSPLYLEIIIIYCTGAFLI 296

Query: 299 SCMLGSVIYYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPS 358
SCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPS
Sbjct: 297 SCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPS 356

Query: 359 RLSSSGTPMLAGVSEYELPEDPRWELPRDRRLVLGKPLGEGCFQGVVLAEAIGLDKDPNR 418
RLSSSGTPMLAGVSEYELPEDPRWELPRDRRLVLGKPLGEGCFQGVVLAEAIGLDKDPNR
Sbjct: 357 RLSSSGTPMLAGVSEYELPEDPRWELPRDRRLVLGKPLGEGCFQGVVLAEAIGLDKDPNR 416

Query: 419 VTKVAVKMLKSDATEKDLSLDIISEMEMMMKMICGHKNIINLLACTQDGPLYVIVEYASKG 478
VTKVAVKMLKSDATEKDLSLDIISEMEMMMKMICGHKNIINLL ACTQDGPLYVIVEYASKG
Sbjct: 417 VTKVAVKMLKSDATEKDLSLDIISEMEMMMKMICGHKNIINLLGACTQDGPLYVIVEYASKG 476

Query: 479 NLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARCMEYLASKKC1IHRDLAAR 538
NLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARCMEYLASKKC1IHRDLAAR
Sbjct: 477 NLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARCMEYLASKKC1IHRDLAAR 536

Query: 539 NVLVTEDNVMKIADEGLARDIHIDYYKKTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFG 598
NVLVTEDNVMKIADEGLARDIHIDYYKKTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFG
Sbjct: 537 NVLVTEDNVMKIADEGLARDIHIDYYKKTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFG 596

Query: 599 VLLWEIFTLGGSPYPGPVVEELFKLLKEGHGRMDKPSNCNTELNYMMMRDCWHAVPSQRPTF 658
VLLWEIFTLGGSPYPGPVVEELFKLLKEGHGRMDKPSNCNTELNYMMMRDCWHAVPSQRPTF
Sbjct: 597 VLLWEIFTLGGSPYPGPVVEELFKLLKEGHGRMDKPSNCNTELNYMMMRDCWHAVPSQRPTF 656

Query: 659 KQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL 718
KQLVE LDRIVALTSNQEYLDLS+PLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL
Sbjct: 657 KQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL 716

Query: 719 PRHPTQLANSGLKRR 733
 PRHP QLAN GLKRR
 Sbjct: 717 PRHPAQLANGGLKRR 731

sp_vs P11362-14 Isoform 15 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 731 AA align
 FGFR1_HUMAN (Human)]

Score = 1420 bits (3677), Expect = 0.0
 Identities = 696/735 (94%), Positives = 709/735 (96%), Gaps = 6/735 (0%)

Query: 1 MWGKCLLFWAVLVATLCTARPAPTLPEQDALPSSEDDDDDSSEEKETDNTKPNV 60
 MW WKCLLFWAVLVATLCTARP+PTLPEQDALPSSEDDDDDSSEEKETDNTKPNV
 Sbjct: 1 MWSWKCLLFWAVLVATLCTARPSTLPEQDALPSSEDDDDDSSEEKETDNTKPNV 60
 Query: 61 APYWTSPKEKMKLHAVPAAKTVFKCPSSGTPNPTLRWLNGKEFKPDHRIGGYKVRYA 120
 APYWTSPKEKMKLHAVPAAKTVFKCPSSGTPNPTLRWLNGKEFKPDHRIGGYKVRYA
 Sbjct: 61 APYWTSPKEKMKLHAVPAAKTVFKCPSSGTPNPTLRWLNGKEFKPDHRIGGYKVRYA 120
 Query: 121 TWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRLQAGLPANKTVALGS 180
 TWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRLQAGLPANKTVALGS
 Sbjct: 121 TWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRLQAGLPANKTVALGS 180
 Query: 181 NVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDNLQPYQILKHSGINSSDAE--VLTLFNV 238
 NVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDNLQPYQILK +C+N++D E VL L NV
 Sbjct: 181 NVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDNLQPYQILKTAGVNNTDKEMEVHLRNV 240
 Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFLI 298
 + +GEY C N IG ++ SANLTV +ALEERPAVMTSPLYLEIIIIYCTGAFLI
 Sbjct: 241 SFEDAGEYTCLAGNSIGLSSHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAFLI 296
 Query: 299 SCMLGSVIIYKMKSGTKSDFSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPS 358
 SCM4-GSVI+YKMKSGTKSDFSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPS
 Sbjct: 297 SCMVGSVIVYKMKSGTKSDFSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPS 356
 Query: 359 RLSSSGTPMLAGVSEYELPEDPRWELPDRDLVLGKPLGEGCFQVVLAEAIGLDKDKPNR 418
 RLSSSGTPMLAGVSEYELPEDPRWELPDRDLVLGKPLGEGCFQVVLAEAIGLDKDKPNR
 Sbjct: 357 RLSSSGTPMLAGVSEYELPEDPRWELPDRDLVLGKPLGEGCFQVVLAEAIGLDKDKPNR 416
 Query: 419 VTKAVAKMLKSDATEKDLSLDLISEMEMMMKMICGHKHNIIINLLACTQDGPLYVIVEYASKG 478
 VTKAVAKMLKSDATEKDLSLDLISEMEMMMKMICGHKHNIIINLLACTQDGPLYVIVEYASKG
 Sbjct: 417 VTKAVAKMLKSDATEKDLSLDLISEMEMMMKMICGHKHNIIINLLACTQDGPLYVIVEYASKG 476
 Query: 479 NLREYLQARRPPGLECYNPNSHNPBOLSSKDLVSCAYQARGMEYLASKKCIRDLAAR 538
 NLREYLQARRPPGLECYNPNSHNPBOLSSKDLVSCAYQARGMEYLASKKCIRDLAAR
 Sbjct: 477 NLREYLQARRPPGLECYNPNSHNPBOLSSKDLVSCAYQARGMEYLASKKCIRDLAAR 536
 Query: 539 NVLVTEDNVMKIADGLARDIHIDYYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFG 598
 NVLVTEDNVMKIADGLARDIHIDYYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFG
 Sbjct: 537 NVLVTEDNVMKIADGLARDIHIDYYKKTTNGRLPVKWMPEALFDRIYTHQSDVWSFG 596
 Query: 599 VLLWEIFTLGGSPYPGPVVEELFKLLKEGHHRMDKPSNCTNELYMMMRDCWHAVPSQRPTF 658
 VLLWEIFTLGGSPYPGPVVEELFKLLKEGHHRMDKPSNCTNELYMMMRDCWHAVPSQRPTF
 Sbjct: 597 VLLWEIFTLGGSPYPGPVVEELFKLLKEGHHRMDKPSNCTNELYMMMRDCWHAVPSQRPTF 656
 Query: 659 KQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL 718
 KQLVE LDRIVALTSNQEYLDLS+PLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPEEPCL
 Sbjct: 657 KQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLPREPCL 716
 Query: 719 PRHPTQLANSGLKRR 733
 PRHP QLAN GLKRR
 Sbjct: 717 PRHPAQLANGGLKRR 731

sp_vs P11362-3 Isoform 6 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 733 AA align
 FGFR1_HUMAN (Human)]

Score = 1415 bits (3664), Expect = 0.0
 Identities = 696/737 (94%), Positives = 709/737 (96%), Gaps = 8/737 (1%)

Query: 1 MWGKCLLFWAVLVATLCTARPAPTLPEQDALPSSEDDDDDSSEEKETDNTKPN-- 58
 MW WKCLLFWAVLVATLCTARP+PTLPEQDALPSSEDDDDDSSEEKETDNTKPN
 Sbjct: 1 MWSWKCLLFWAVLVATLCTARPSTLPEQDALPSSEDDDDDSSEEKETDNTKPNRM 60
 Query: 59 PVAPYWTSPKEKMKLHAVPAAKTVFKCPSSGTPNPTLRWLNGKEFKPDHRIGGYKVR 118
 PVAPYWTSPKEKMKLHAVPAAKTVFKCPSSGTPNPTLRWLNGKEFKPDHRIGGYKVR
 Sbjct: 61 PVAPYWTSPKEKMKLHAVPAAKTVFKCPSSGTPNPTLRWLNGKEFKPDHRIGGYKVR 120
 Query: 119 YATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRLQAGLPANKTVAL 178
 YATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRLQAGLPANKTVAL
 Sbjct: 121 YATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRLQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIOWLKHIEVNGSKIGPDNL PYVQILKHSGINSSDAE--VLTLF 236
 GSNVEFMCKVYSDPQPHIOWLKHIEVNGSKIGPDNL PYVQILK +G+N++D E VL L
 Sbjct: 181 GSNVEFMCKVYSDPQPHIOWLKHIEVNGSKIGPDNL PYVQILKTAGVNNTDKEMEVHLR 240

Query: 237 NVTAEQSGEYVCKVSNVYIGEANQSAWLTVTRPAKALEERPAVMTSPLYLEIIIIYCTGAF 296
 NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAF
 Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGLGSVI1YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
 LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR
 Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDP 416
 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDP
 Sbjct: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDP 416

Query: 417 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLACTQDGPLYVIVEYAS 476
 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLL ACTQDGPLYVIVEYAS
 Sbjct: 417 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLGACTQDGPLYVIVEYAS 476

Query: 477 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLA 536
 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLA
 Sbjct: 477 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLA 536

Query: 537 ARNVLVTEDNVMKIADFGLARDIHIDYYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596
 ARNVLVTEDNVMKIADFGLARDIHIDYYKKTNGRLPVKWMPEALFDRIYTHQSDVWS
 Sbjct: 537 ARNVLVTEDNVMKIADFGLARDIHIDYYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596

Query: 597 FGVLLWEIFTLGSPYPGPVVEELFKLLKEGHMDKPSNCTNELYMMMRDCWHAVPSQR 656
 FGVLLWEIFTLGSPYPGPVVEELFKLLKEGHMDKPSNCTNELYMMMRDCWHAVPSQR 656
 Sbjct: 597 FGVLLWEIFTLGSPYPGPVVEELFKLLKEGHMDKPSNCTNELYMMMRDCWHAVPSQR 656

Query: 657 TFKQLVEVLDRAVALTSNQEYLDLS+PLDQYSPSFDPDRSSTCSCSGEDSVFSHEPLPEEP 716
 TFKQLVE LDRVALTSNQEYLDLS+PLDQYSPSFDPDRSSTCSCSGEDSVFSHEPLPEEP
 Sbjct: 657 TFKQLVEDLDRVALTSNQEYLDLSMPLDQYSPSFDPDRSSTCSCSGEDSVFSHEPLPEEP 716

Query: 717 CLPRHPTQLANSGLKRR 733
 CLPRHP QLAN GLKRR
 Sbjct: 717 CLPRHPAQLANGGLKRR 733

sp_vs P11362-4 Isoform 8 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 731 AA align
 FGFR1_HUMAN (Human)]

Score = 1407 bits (3642), Expect = 0.0
 Identities = 694/737 (94%), Positives = 707/737 (95%), Gaps = 10/737 (1%)

Query: 1 MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPN-- 58
 MW WKCLLFWAVLVTATLCTARP+PTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPN
 Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNRM 60

Query: 59 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRLWLNKGKEFKPDHHRIGGYKVR 118
 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRLWLNKGKEFKPDHHRIGGYKVR
 Sbjct: 61 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRLWLNKGKEFKPDHHRIGGYKVR 120

Query: 119 YATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVAL 178
 YATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVAL
 Sbjct: 121 YATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIOWLKHIEVNGSKIGPDNL PYVQILKHSGINSSDAE--VLTLF 236
 GSNVEFMCKVYSDPQPHIOWLKHIEVNGSKIGPDNL PYVQILK +G+N++D E VL L
 Sbjct: 181 GSNVEFMCKVYSDPQPHIOWLKHIEVNGSKIGPDNL PYVQILKTAGVNNTDKEMEVHLR 240

Query: 237 NVTAEQSGEYVCKVSNVYIGEANQSAWLTVTRPAKALEERPAVMTSPLYLEIIIIYCTGAF 296
 NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAF
 Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGLGSVI1YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
 LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVR
 Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV --SADSSASMNSGVLLVR 354

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDP 416
 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDP
 Sbjct: 355 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDP 414

Query: 417 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLACTQDGPLYVIVEYAS 476
 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLL ACTQDGPLYVIVEYAS
 Sbjct: 415 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLGACTQDGPLYVIVEYAS 474

Query: 477 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLA 536
 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLA
 Sbjct: 475 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLA 534

Query: 537 ARNVLVTEDNVMKIADFGLARDIHIDYYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596

ARNVLVTEDNVMKIADFGLARDIHHIDYYKTTNGRLPVKWMPEALFDRIYTHQSDVWS
 Sbjct: 535 ARNVLVTEDNVMKIADFGLARDIHHIDYYKTTNGRLPVKWMPEALFDRIYTHQSDVWS 594

Query: 597 FGVLLWEIFTLGSPYPGVPVEELFKLLKEGHMDKPSNCTNELYMMMRDCWHAVPSQR 656
 FGVLWWEIFTLGSPYPGVPVEELFKLLKEGHMDKPSNCTNELYMMMRDCWHAVPSQR 654

Sbjct: 595 FGVLLWEIFTLGSPYPGVPVEELFKLLKEGHMDKPSNCTNELYMMMRDCWHAVPSQR 654

Query: 657 TPKQLVEVLDRIALTSNQEYLDSIPLDQYSFSPDTRSSTCSSGEDSVFSHEPLPEEP 716
 TPKQLVE LDRIVALTSNQEYLDS+PLDQYSFSPDTRSSTCSSGEDSVFSHEPLPEEP 716

Sbjct: 655 TPKQLVEDLDRIVALTSNQEYLDSMPLDQYSFSPDTRSSTCSSGEDSVFSHEPLPEEP 714

Query: 717 CLPRHPTQLANGLKRR 733
 CLPRHP QLAN GLKRR

Sbjct: 715 CLPRHPAQLANGGLKRR 731

sp_vs P11362-7 Isoform 14 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 820 AA
 FGFR1_HUMAN (Human)] align

Score = 1357 bits (3513), Expect = 0.0
 Identities = 668/705 (94%), Positives = 680/705 (96%), Gaps = 6/705 (0%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS
 Sbjct: 120 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 179

Query: 91 GTPNPTRLWLKGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGSINH 150
 GTPNPTRLWLKGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGSINH
 Sbjct: 180 GTPNPTRLWLKGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGSINH 239

Query: 151 TYQLDVVERSPHPRPILQAGLPANKTVALGSNEFMCKVYSDPOPHIQWLKHIEVNGSKIG 210
 TYQLDVVERSPHPRPILQAGLPANKTVALGSNEFMCKVYSDPOPHIQWLKHIEVNGSKIG
 Sbjct: 240 TYQLDVVERSPHPRPILQAGLPANKTVALGSNEFMCKVYSDPOPHIQWLKHIEVNGSKIG 299

Query: 211 PDNLPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTTRP 268
 PDNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLT
 Sbjct: 300 PDNLPYVQILKTAGVNNTDKEMEVHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL-- 357

Query: 269 VAKALEERPAVMTPSPLYLEIIYICTGAFLISCMGLSVIYKMKSGTKKSDFHQSMAVHKL 328
 +ALEERPAVMTPSPLYLEIIYICTGAFLISCM+GSVI+YKMKSGTKKSDFHQSMAVHKL
 Sbjct: 358 --EALEERPAVMTPSPLYLEIIYICTGAFLISCMVGSVIVYKMKSGTKKSDFHQSMAVHKL 415

Query: 329 AKSIPLRQRQTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 388
 AKSIPLRQRQTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR
 Sbjct: 416 AKSIPLRQRQTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 475

Query: 389 LVLGKPLGECCFGVVLAEAIGLDKDPNVRTKAVAKMLKSDATEKDLSLDIISEMEMMKM 448
 LVLGKPLGECCFGVVLAEAIGLDKDPNVRTKAVAKMLKSDATEKDLSLDIISEMEMMKM
 Sbjct: 476 LVLGKPLGECCFGVVLAEAIGLDKDPNVRTKAVAKMLKSDATEKDLSLDIISEMEMMKM 535

Query: 449 IGHKHNIIINLLACTQDGPLYVIVEYASKGNLREYLQARRPGLEYCYNPSHNPEEQLSS 508
 IGHKHNIIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPGLEYCYNPSHNPEEQLSS
 Sbjct: 536 IGHKHNIIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPGLEYCYNPSHNPEEQLSS 595

Query: 509 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT 568
 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT
 Sbjct: 596 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT 655

Query: 569 TNGRLPVKWMPEALFDRIYTHQSDVVSFGVLLWEIFTLGSPYPGVPVEELFKLLKEGH 628
 TNGRLPVKWMPEALFDRIYTHQSDVVSFGVLLWEIFTLGSPYPGVPVEELFKLLKEGH
 Sbjct: 656 TNGRLPVKWMPEALFDRIYTHQSDVVSFGVLLWEIFTLGSPYPGVPVEELFKLLKEGH 715

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQIIVEVLDRIALTSNQEYLDSIPLDQYS 688
 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQIIVEVLDRIALTSNQEYLDS+PLDQYS
 Sbjct: 716 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQIIVEVLDRIALTSNQEYLDSMPLDQYS 775

Query: 689 PSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANGLKRR 733
 PSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
 Sbjct: 776 PSFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

Score = 91.3 bits (225), Expect = 5e-18
 Identities = 78/305 (25%), Positives = 118/305 (38%), Gaps = 81/305 (26%)

Query: 1 MWGWKCLLFWAFLVTATLCTARPATLPEQDALPSSSEDDDDSSSEEKETDNTKPNPV 60
 MW WKCLLFWAFLVTATLCTARP+PTLPEQ----- 30

Sbjct: 1 MWSWKCLLFWAFLVTATLCTARPSTLPEQ----- 30

Query: 61 APYWTSPPEKMEKKLHAVPAAKTVKFKCPSSGTNPTRLWLKGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 31 AQPGWAPVEVESFL--VHPGDLQLRCRRLDDVQ-SINLRDGVQLAESNR----TRIT 82

Query: 121 TWSIIMDSVVPDKGNYTCIVENEYGSINHTYQLDVVERSPH----- 162
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPGSDTYYFSVNVS DALPSSSEDDDDSSSEEKETD 142

Query: 163 ----RPILQAGLPANK-----TVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
 P+ K V V+F C P P ++WLK NG + PD
 Sbjct: 143 NTKPNPVAPYWTSSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLK---NGKEFKPD 198

Query: 213 NLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----R 267
 + + + + + + + + + + G Y C V N G N + L V R
 Sbjct: 199 HRIGGYKVRYATWS-----IIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVVERSPHR 252

Query: 268 PVAKA 272
 P+ +A
 Sbjct: 253 PILQA 257

sp_P11362 Basic fibroblast growth factor receptor 1 precursor (EC 2.7.10.1) 822 AA
 FGFR1_HUMAN (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase 2) (c-fgr)
 (CD331 antigen) [FGFR1] [Homo sapiens (Human)]

Score = 1352 bits (3500), Expect = 0.0
 Identities = 668/707 (94%), Positives = 680/707 (96%), Gaps = 8/707 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPN--PVAPYWTSSPEKMEKKLHAVPAAKTVFKCP 88
 DALPSSSEDDDDDDSSSEEKETDNTKPN PVAPYWTSSPEKMEKKLHAVPAAKTVFKCP
 Sbjct: 120 DALPSSSEDDDDDDSSSEEKETDNTKPNRMPVAPYWTSSPEKMEKKLHAVPAAKTVFKCP 179

Query: 89 SSCTPNPTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSI 148
 SSCTPNPTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSI
 Sbjct: 180 SSCTPNPTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVERSPHRILOQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
 NHTYQLDVERSPHRILOQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVERSPHRILOQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDNLPVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
 IGPDNLPVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDNLPVQILKTAGVNLTDEMEVLHLRNVSFEDAGEYTCLAGNSICLSHHSAWLTVL 359

Query: 267 RPVAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMLCSVIYKMKSGTKKSDFHQSMAVH 326
 +ALEERPAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHQSMAVH
 Sbjct: 360 ----EALEERPAVMTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHQSMAVH 415

Query: 327 KLAISIPLRRQRTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAISIPLRRQRTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAISIPLRRQRTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 475

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMM 446
 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMM
 Sbjct: 476 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMM 535

Query: 447 KMIGHKNNIINLLACTQDGPLYVIVEYASKGNLREYLQARPPGLECYCYNPSHNPEEQL 506
 KMIGHKNNIINLL ACTQDGPLYVIVEYASKGNLREYLQARPPGLECYCYNPSHNPEEQL
 Sbjct: 536 KMIGHKNNIINLLACTQDGPLYVIVEYASKGNLREYLQARPPGLECYCYNPSHNPEEQL 595

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMIADFGLARDIH HIDYYK 566
 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMIADFGLARDIH HIDYYK
 Sbjct: 596 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMIADFGLARDIH HIDYYK 655

Query: 567 KTNGLRPLVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE 626
 KTNGLRPLVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE
 Sbjct: 656 KTNGLRPLVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE 715

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLS+PLDQ 686
 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE VLDRIVALTSNQEYLDLS+PLDQ
 Sbjct: 716 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLS+PLDQ 775

Query: 687 YSPSPFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANGLKRR 733
 YSPSPFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
 Sbjct: 776 YSPSPFPDTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 822

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAFLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNPV 60
 MW WKCLLFWAFLVLTATLCTARP+PTLPEQ
 Sbjct: 1 MWSWKCLLFWAFLVLTATLCTARPSPTLPEQ----- 30

Query: 61 APYWTSSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL+G + +R R
 Sbjct: 31 AQPWGAPVEVESFL--VHPGDLQLQRCLRRLRDVQ-SINWLRDGVOLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVVERSP----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDDTTYSVNVSDLPSSEDDDDDDSSSEEKTD 142

Query: 162 ----H R P I L Q A G L P A N K -----T V A L G S N V E F M C K V Y S D P Q P H I Q W L K H I E V N G S K I G 210
 P+ K V V+F C P P ++WLK NG +
 Sbjct: 143 N T K P N R M P V A P Y W T S P E K M E K K L H A V P A A K T V K F K C P S G T P N P T L R W L K ----N G K E F K 198

Query: 211 P D N L P Y V Q I L K H S G I N S S D E A V L T L F N V T E A Q S G E Y V C K V S N Y I G E A N Q S A W L T V T ----- 266
 P D + + + + + + + + + V + G Y C V N G N + L V
 Sbjct: 199 P D H R I G G Y K V R Y A T W S -----I I M D S V V P S D K G N Y T C I V E N E Y G S I N H T Y Q L D V V E R S P 252

Query: 267 -R P V A K A 272
 R P + + A
 Sbjct: 253 H R P I L Q A 259

tr Q53H63 Fibroblast growth factor receptor 1 isoform 2 variant (Fragment) 820 AA
 Q53H63_HUMAN [Homo sapiens (Human)] align

Score = 1351 bits (3496), Expect = 0.0
 Identities = 665/705 (94%), Positives = 678/705 (96%), Gaps = 6/705 (0%)

Query: 31 D A L P S S E D D D D D D S S E E K E T D N T K P N P V A P Y W T S P E K M E K K L H A V P A A K T V K F K C P S S 90
 DALPSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVFKCPSS 179

Query: 91 G T P N P T L R W L K N G K E F K P D H R I G G Y K V R Y A T W S I I M D S V V P S D K G N Y T C I V E N E Y G S I N H 150
 GTPNPTRLWLNKGKEFPDKPHRIGGYKVRYATWSIIMDSVVP DKGNYTCIVENEYGSINH
 Sbjct: 180 G T P N P T L R W L K N G K E F K P D H R I G G Y K V R Y A T W S I I M D S V V P F D K G N Y T C I V E N E Y G S I N H 239

Query: 151 T Y Q L D V V E R S P H R P I L Q A G L P A N K T V A L G S N V E F M C K V Y S D P Q P H I Q W L K H I E V N G S K I G 210
 TYQLDVVERSPHRPILQAGLPANKTVALGSNEFMCVKYSDPQPHIQWLKHIEVNGSKIG
 Sbjct: 240 T Y Q L D V V E R S P H R P I L Q A G L P A N K T V A L G S N V E F M C K V Y S D P Q P H I Q W L K H I E V N G S K I G 299

Query: 211 P D N L P Y V Q I L K H S G I N S S D E A E - V L T L F N V T E A Q S G E Y V C K V S N Y I G E A N Q S A W L T V T R P 268
 PDNLPYVQILK +G+N++D E VL L NV+ +GBY C N IG ++ SAWLT
 Sbjct: 300 P D N L P Y V Q I L K T A G V N T T D K E M E V L H L R N V S P E D A G E Y T C L A G N S I G L S H H S A W L T V L -- 357

Query: 269 V A K A L E E R P A V M T S P L Y L E I I I Y C T G A F L I S C M L G S V I I Y K M K S G T K K S D F H S Q M A V H X L 328
 +A E A L E E R P A V M T S P L Y L E I I I Y C T G A F L I S C M + G S V I + Y K M K S G T K K S D F H S Q M A V H X L
 Sbjct: 358 --E A L E E R P A V M T S P L Y L E I I I Y C T G A F L I S C M V G S V I V Y K M K S G T K K S D F H S Q M A V H X L 415

Query: 329 A K S I P L R R Q V T V S A D S S A S M N S G V L L V R P S R L S S S G T P M L A G V S E Y E L P E D P R W E L P R D R 388
 AKSIPLRQQVTVSADSSASMSNSGVLLVRPSRLSSSGTFMLAGVSEYELPEDPRWELPRDR
 Sbjct: 416 A K S I P L R R Q V T V S A D S S A S M N S G V L L V R P S R L S S S G T P M L A G V S E Y E L P E D P R W E L P R D R 475

Query: 389 L V I G K P L G E G C F Q V V L A E A I G L D K D K P N R V T K V A V K M L K S D A T E K D L S D L I S E M E M M K M 448
 LVIG+PLGEGCFGQVVLAAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLI SEMEMMKM
 Sbjct: 476 L V I G R P L G E G C F Q V V L A E A I G L D K D K P N R V T K V A V K M L K S D A T E K D L S D L I S E M E M M K M 535

Query: 449 I G K H K N I I N L L E A C T Q D G P L Y V I V E Y A S K G N I R E Y L Q A R R P P G L E Y C Y N P S H N P E E Q L S S 508
 IGHKHNIIINLL ACTQDGPLYVIVIVEYASKGNLREYLQA RPPGLEYCYNPSHNPEEQQLSS
 Sbjct: 536 I G K H K N I I N L L G A C T Q D G P L Y V I V E Y A S K G N L R E Y L Q A W R P P G L E Y C Y N P S H N P E E Q L S S 595

Query: 509 K D L V S C A Y Q V A R G M E Y L A S K K C I H R D L A A R N V L V T E D N V M K I A D F G L A R D I H H I D Y Y K K T 568
 KDLVSCAYQVARGMEMYLASKKCIIHRDLAARNVLVTEDNVMKIADFGLARDIHHDYYKKT
 Sbjct: 596 K D L V S C A Y Q V A R G M E Y L A S K K C I H R D L A A R N V L V T E D N V M K I A D F G L A R D I H H I D Y Y K K T 655

Query: 569 T N G R L P V K W M A P E A L F D R I Y T H Q S D V W S F G V I L L W E I F T L G G S P Y P G V P V E E L F K L L K E G H 628
 TNGLRPLVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPPYPGVPVEELFKLLKEGH
 Sbjct: 656 T N G R L P V K W M A P E A L F D R I Y T H Q S D V W S F G V I L L W E I F T L G G S P Y P G V P V E E L F K L L K E G H 715

Query: 629 R M D K P S N C T N E L Y M M M R D C W H A V P S Q R P T F K Q L V E V L D R I V A L T S N Q E Y L D L S I P L D Q Y S 688
 RMDKPSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLS+PLDQYS
 Sbjct: 716 R M D K P S N C T N E L Y M M M R D C W H A V P S Q R P T F K Q L V E D L D R I V A L T S N Q E Y L D L S M P L D Q Y S 775

Query: 689 P S F P D T R S S T C S S G E D S V F S H E P L P E E P C L P R H P T Q L A N G L K R R 733
 PSFPDTRSSTCSSEGDSVFSHEPLPEEPCLPRHP QLAN GLKRR
 Sbjct: 776 P S F P D T R S S T C S S G E D S V F S H E P L P E E P C L P R H P A Q L A N G L K R R 820

Score = 90.1 bits (222), Expect = 1e-17
 Identities = 78/305 (25%), Positives = 117/305 (38%), Gaps = 81/305 (26%)

Query: 1 M W G W K C L L F W A V L V T A T L C T A R P A P T L P E Q D A L P S S E D D D D D S S E E K E T D N T K P N P V 60
 MW WKCLLFWAFLVTATLC TARP+PTLPEQ
 Sbjct: 1 M W S W K C L L F W A V L V T A T L C T A R P S P T L P E Q ----- 30

Query: 61 A P Y W T S P E K M E K K L H A V P A A K T V K F K C P S S G T P N P T L R W L K N G K E F K P D H R I G G Y K V R Y A 120
 A W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 31 A Q P W G A P V E V E S F L --V H P G D L L Q L R C R L R D D V Q -S I N W L R D G V Q L A E S N R -----TRIT 82

Query: 121 T W S I I M D S V V P S D K G N Y T C I V E N E Y G S I N H T Y Q L D V V E R S P H ----- 162
 + + VP+D G Y C + + GS + ++V + P
 Sbjct: 83 G E E V E V Q D S V P A D S G L Y A C V T S S P S G S D T T Y F S V N V S D A L P S S E D D D D D S S S E E K E T D 142

Query: 163 ----R P I L Q A G L P A N K -----T V A L G S N V E F M C K V Y S D P Q P H I Q W L K H I E V N G S K I G P D 212
 P+ K V V+F C P P ++WLK NG + PD

Sbjct: 143 NTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPD 198
 Query: 213 NL PYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----R 267
 + + + + + + + + V G Y C V N G N + L V R
 Sbjct: 199 HRIGGYKVRYATWS-----IIMDSVVPFDKGNYTCIVENEYGSINHTYQLDVERSPHR 252
 Query: 268 PVAKA 272
 P+ +A
 Sbjct: 253 PILQA 257

tr Q59H40 Fibroblast growth factor receptor 1 isoform 1 variant (Fragment) 814 AA
 Q59H40_HUMAN [Homo sapiens (Human)] align

Score = 1344 bits (3478), Expect = 0.0
 Identities = 666/707 (94%), Positives = 678/707 (95%), Gaps = 10/707 (1%)

Query: 31 DALPSSEDDDDDDSSSEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSEDDDDDDSSSEEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 114 DALPSSEDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 173
 Query: 89 SSCTPNPTLRLWLNKGKEFPDKPHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSI 148
 SSCTPNPTLRLWLNKGKEFPDKPHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSI
 Sbjct: 174 SSCTPNPTLRLWLNKGKEFPDKPHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSI 233
 Query: 149 NHTYQLDVERSPHRIQLQAGLPANKTVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSK 208
 NHTYQLDVERSPHRIQLQAGLPANKTVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSK
 Sbjct: 234 NHTYQLDVERSPHRIQLQAGLPANKTVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSK 293
 Query: 209 IGPDPNLPYVQIILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
 IGPDPNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 294 IGPDPNLPYVQIILTAGVNNTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHSAWLTVL 353
 Query: 267 RPVAKAELERPAVMTSPLYLEIIIIYCTGAFLISCMILGSVIYKMKSGTJKSDFHSQMAVH 326
 +ALEERPAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTJKSDFHSQMAVH
 Sbjct: 354 --EAELEERPAVMTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMKSGTJKSDFHSQMAVH 409
 Query: 327 KLAKSIPLRQQTVVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAKSIPLRQQV SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 410 KLAKSIPLRQQV--SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 467
 Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM
 Sbjct: 468 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 527
 Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCNPSPHNPEEQL 506
 KMIGKHKNIINL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCNPSPHNPEEQL
 Sbjct: 528 KMIGKHKNIINL GACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCNPSPHNPEEQL 587
 Query: 507 SSKDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMIADFGLARDIHIDYYK 566
 SSKDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMIADFGLARDIHIDYYK
 Sbjct: 588 SSKDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMIADFGLARDIHIDYYK 647
 Query: 567 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE 626
 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE
 Sbjct: 648 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE 707
 Query: 627 GHRMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVEVLDRIALTSNQEYLDLSIPLDQ 686
 GHRMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVE LDRIALTSNQEYLDLS+PLDQ
 Sbjct: 708 GHRMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVEDLDRIALTSNQEYLDLSMPLDQ 767
 Query: 687 YSPSFPTDRSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
 YSPSFPTDRSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
 Sbjct: 768 YSPSFPTDRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 814

Score = 43.1 bits (100), Expect = 0.002
 Identities = 49/244 (20%), Positives = 88/244 (36%), Gaps = 53/244 (21%)

Query: 64 WTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWS 123
 W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 28 WGAPVEVESFL--VHPGDLLQLRCRLRDDVQ-SINWL RDGVQLAESNR----TRITGEE 79
 Query: 124 IIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVERSP----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 80 VEVQDSVPADSGLYACVTSSPGSDTTYSFNVSDALPSSEDDDDDDSSSEEKETDNTK 139
 Query: 162 --HRPILQAGLPANK-----TVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSKIGPDN 213
 P+ K V V+F C P P ++WLK NG + PD+
 Sbjct: 140 PNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPDH 195
 Query: 214 LPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----RP 268
 + + + + + + + + V + G Y C V N G N + L V R P
 Sbjct: 196 RIGGYKVRYATWS-----IIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVERSPHRP 249

Query: 269 VAKA 272
 + +A
 Sbjct: 250 ILQA 253

sp_vs P11362-2 Isoform 4 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 820 AA align
 FGFR1_HUMAN (Human)]

Score = 1344 bits (3478), Expect = 0.0
 Identities = 666/707 (94%), Positives = 678/707 (95%), Gaps = 10/707 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSSEDDDDDDSSSEEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 120 DALPSSSEDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSCTPNPTLRLWLNKEFKPDKHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGS 148
 SSCTPNPTLRLWLNKEFKPDKHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGS 148
 Sbjct: 180 SSCTPNPTLRLWLNKEFKPDKHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGS 239

Query: 149 NHTYQLDVERSPHRPIQAGLPANKTVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSK 208
 NHTYQLDVERSPHRPIQAGLPANKTVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVERSPHRPIQAGLPANKTVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSK 299

Query: 209 IGPDNLPVQILKHSGINSSDAE--VLTLFNVTEAQSCHEYVCKVSNYIGEANQSAWLTV 266
 IGPDNLPVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDNLPVQILKTAGVNNTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSSHSAWLTVL 359

Query: 267 RPVAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMGLSVIYKMKSGTJKSDFHSQMAVH 326
 +ALEERPAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTJKSDFHSQMAVH
 Sbjct: 360 ---EALEERPAVMTSPLYLEIIIIYCTGAFLISCMVGIVVYKMKSGTJKSDFHSQMAVH 415

Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSSLSSGTTPMLAGVSEYELPEDPRWELPR 386
 KLAKSIPLRQV SADSSASMNSGVLLVRPSSLSSGTTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAKSIPLRQV---SADSSASMNSGVLLVRPSSLSSGTTPMLAGVSEYELPEDPRWELPR 473

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDISEMEMM 446
 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDISEMEMM
 Sbjct: 474 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDISEMEMM 533

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPGLLEYCYNPSHNPSEEQL 506
 KMIGKHKNIINL ACTQDGPLYVIVEYASKGNLREYLQARRPGLLEYCYNPSHNPSEEQL
 Sbjct: 534 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPGLLEYCYNPSHNPSEEQL 593

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMIADFGLARDIHIDYYK 566
 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMIADFGLARDIHIDYYK
 Sbjct: 594 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMIADFGLARDIHIDYYK 653

Query: 567 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVVEELFKLLKE 626
 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVVEELFKLLKE
 Sbjct: 654 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVVEELFKLLKE 713

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSPQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
 GHRMDKPSNCTNELYMMMRDCWHAVPSPQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQ
 Sbjct: 714 GHRMDKPSNCTNELYMMMRDCWHAVPSPQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQ 773

Query: 687 YSPSFPTRSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
 YSPSFPTRSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
 Sbjct: 774 YSPSFPTRSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGKCLLPWAFLVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNPV 60
 MW WKCLLPWAFLVTATLCTARP+PTLPEQ----- 30
 Sbjct: 1 MWSWKCLLPWAFLVTATLCTARPSPFTLPEQ----- 30

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFCKPSSGTPNPTLRLWLNKGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 31 AQPGWAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWL RDGVQLAESNR----TRIT 82

Query: 121 TWSIIMDSVVPSDKGNYTCIVENEYGSINHHTYQLDVVERSP----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSCSDTYYFSVNVS DALPSSSEDDDDDDSSSEEKETD 142

Query: 162 ----HRPILQAGLPANK----TVALGSNVEFMCKVYSDPQPHIQOWLKHIEVNGSKIG 210
 P+ K V V+F C P P ++WLK NG +
 Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFCKPSSGTPNPTLRLWLK----NGKEFK 198

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT---- 266
 PD+ +++ + + + +V + G Y C V N G N + L V
 Sbjct: 199 PDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHHTYQLDVVERSP 252

Query: 267 -RPVAKA 272
 RP+ +A

Sbjct: 253 HRPILQA 259

sp_vs P11362-5 Isoform 10 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 662 AA align
FGFR1_HUMAN (Human)]

Score = 1275 bits (3299), Expect = 0.0
Identities = 629/666 (94%), Positives = 641/666 (96%), Gaps = 6/666 (0%)

Query: 70 MEKKLHAVPAAKTVFKCPSSGTNPTRLWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129
MEKKLHAVPAAKTVFKCPSSGTNPTRLWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV
Sbjct: 1 MEKKLHAVPAAKTVFKCPSSGTNPTRLWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 189
VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY
Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKHSGINSSDAE--VLTLFNVTTEAQSGEYV 247
SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILK +G+N++D E VL L NV+ +GEY
Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKTAGVNNTDKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVPRAKALEERPAVMTSPLYLEIIYYCTGAFLISCMLGSVII 307
C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIYYCTGAFLISCM+GSVI+
Sbjct: 181 CLAGNSIGLSHHSAWLTVL---EALEERPAVMTSPLYLEIIYYCTGAFLISCMVGIV 236

Query: 308 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMMSGVLLVRPSPRLSSSGTPM 367
YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMMSGVLLVRPSPRLSSSGTPM
Sbjct: 237 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMMSGVLLVRPSPRLSSSGTPM 296

Query: 368 LAGVSEYELPEDPRWELPRDRVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
LAGVSEYELPEDPRWELPRDRVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML
Sbjct: 297 LAGVSEYELPEDPRWELPRDRVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 356

Query: 428 KSDATEKDLSDLISEMEMMMKMIKGHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
KSDATEKDLSDLISEMEMMMKMIKGHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR
Sbjct: 357 KSDATEKDLSDLISEMEMMMKMIKGHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 416

Query: 488 RPPGLECYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKCIHRLAARNVLVTEDNV 547
RPPGLECYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKCIHRLAARNVLVTEDNV
Sbjct: 417 RPPGLECYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKCIHRLAARNVLVTEDNV 476

Query: 548 MKIADFGGLARDIHHIDYYKKTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFGVLLWEIFTL 607
MKIADFGGLARDIHHIDYYKKTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFGVLLWEIFTL
Sbjct: 477 MKIADFGGLARDIHHIDYYKKTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFGVLLWEIFTL 536

Query: 608 GGSPYPGVVPVEELFKLLKEGHRMKDPKSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDR 667
GGSPYPGVVPVEELFKLLKEGHRMKDPKSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDR
Sbjct: 537 GGSPYPGVVPVEELFKLLKEGHRMKDPKSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDR 596

Query: 668 IVALTSNQEYLDLSIPLDQYSPSFPDTRSSCTSGGEDSVFSHEPLPEEPCLPRHPTQLAN 727
IVALTSNQEYLDLSIPLDQYSPSFPDTRSSCTSGGEDSVFSHEPLPEEPCLPRHPTQLAN
Sbjct: 597 IVALTSNQEYLDLSIPLDQYSPSFPDTRSSCTSGGEDSVFSHEPLPEEPCLPRHPTQLAN 656

Query: 728 SGLKRR 733
GLKRR
Sbjct: 657 GGLKRR 662

sp_vs P11362-6 Isoform 12 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 660 AA align
FGFR1_HUMAN (Human)]

Score = 1266 bits (3277), Expect = 0.0
Identities = 627/666 (94%), Positives = 639/666 (95%), Gaps = 8/666 (1%)

Query: 70 MEKKLHAVPAAKTVFKCPSSGTNPTRLWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129
MEKKLHAVPAAKTVFKCPSSGTNPTRLWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV
Sbjct: 1 MEKKLHAVPAAKTVFKCPSSGTNPTRLWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 189
VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY
Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKHSGINSSDAE--VLTLFNVTTEAQSGEYV 247
SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILK +G+N++D E VL L NV+ +GEY
Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKTAGVNNTDKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVPRAKALEERPAVMTSPLYLEIIYYCTGAFLISCMLGSVII 307
C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIYYCTGAFLISCM+GSVI+
Sbjct: 181 CLAGNSIGLSHHSAWLTVL---EALEERPAVMTSPLYLEIIYYCTGAFLISCMVGIV 236

Query: 308 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMMSGVLLVRPSPRLSSSGTPM 367

YKMKSGTCKSDPHSQMAVHKLAKSIPLRQV SADSSASMNSGVLLVRPSRLSSSGTPM
 Sbjct: 237 YKMKSGTCKSDPHSQMAVHKLAKSIPLRQV--SADSSASMNSGVLLVRPSRLSSSGTPM 294
 Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
 LAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDKPNRVTKVAVKML
 Sbjct: 295 LAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDKPNRVTKVAVKML 354
 Query: 428 KSDATEKDLSDLISEMEMMMKMGKHKNIINLLAEACTQDGPLYVIVEYASKGNLREYLQAR 487
 KSDATEKDLSDLISEMEMMMKMGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR
 Sbjct: 355 KSDATEKDLSDLISEMEMMMKMGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 414
 Query: 488 RPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCICHRDLAARNVLVTEDNV 547
 RPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCICHRDLAARNVLVTEDNV
 Sbjct: 415 RPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCICHRDLAARNVLVTEDNV 474
 Query: 548 MKIADFGGLARDIHHIDYYKKTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTL 607
 MKIADFGGLARDIHHIDYYKKTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTL
 Sbjct: 475 MKIADFGGLARDIHHIDYYKKTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTL 534
 Query: 608 GGSPPGVPVEELFKLLKECHRMKDPKSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEVLD 667
 GGSPPGVPVEELFKLLKECHRMKDPKSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEVLD
 Sbjct: 535 GGSPPGVPVEELFKLLKECHRMKDPKSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEDLDR 594
 Query: 668 IVALTSNQEYLDLSIPLDQYSPSFPPDTRSSCTSSGEDSVFSHEPLPEEPCLPRHPTQLAN 727
 IVALTSNQEYLDLS+PLDQYSPSFPPDTRSSCTSSGEDSVFSHEPLPEEPCLPRHPTQLAN
 Sbjct: 595 IVALTSNQEYLDLSMPLDQYSPSFPPDTRSSCTSSGEDSVFSHEPLPEEPCLPRHPTQLAN 654
 Query: 728 SGKRR 733
 GLKRR
 Sbjct: 655 GGLKRR 660

sp_vs P21802-3 Isoform 3 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 822 AA
 FGFR2_HUMAN (Human)] align

Score = 1108 bits (2867), Expect = 0.0
 Identities = 537/694 (77%), Positives = 606/694 (87%), Gaps = 7/694 (1%)
 Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
 DA+ S +D+DD D+ E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISGGDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182
 Query: 91 GTPNPNTLRLKGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINH 150
 G P PT+RWLKGKEF+HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKGKEFKPQEHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVENEYGSINH 242
 Query: 151 TYOLDVVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW-KH+E NGSK G
 Sbjct: 243 TYHLDVVVERSPHRPILQAGLPANASTVVGGDEVFCKVYSDAQPHIQWIKIHEVNGSKIG 302
 Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNVIGEANQSAWLTVTRPVA 270
 PD LPY++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNVIG+ANQSAWLTV P
 Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLALFNVTEADAGEYICKVSNVIGQANQSAWLTVL-PKQ 361
 Query: 271 KALEERPAVMSPPLYLEIIYCTGAFLISCMGLSVIYKMKSGTKSDPHSQMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DE SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDPYLEIAIYICIGVFLIACMVVTVILCRMNTKKPDFSSQPAVHKLTK 421
 Query: 331 IPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSAEESSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWEFPDRK 481
 Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMMK 448
 L LGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMMK
 Sbjct: 482 LTIGKPLGEGCFGQVVMABAVGIDKDKPKEAFTVAVKMLKDDATEKDLSDLVSEMEMMMK 541
 Query: 449 IGKHKNIINLLAEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSS 508
 IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
 Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601
 Query: 509 KDLVSCAYQVARGMEYLASKKCICHRDLAARNVLVTEDNVMIKIADEFGGLARDIHHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS-KCICHRDLAARNVLVTE-NVMKIADFGGLARDI++IDYYKKT
 Sbjct: 602 KDLVSCTYQLARGMEYLASKKCICHRDLAARNVLVTEENNVMKIADFGGLARDINNIDYYKKT 661
 Query: 569 TNGLRPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGH 628
 TNGLRPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKEGH
 Sbjct: 662 TNGLRPVKWMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721
 Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDIVALTSNQEYLDLSIPLDQYS 688
 RMDK+ +NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYS
 Sbjct: 722 RMDK PANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNEEYLDLSQPLEQYS 781
 Query: 689 PSFPDTRSSCTSSGEDSVFSHEPLPEEPCLPRHPT 722
 PS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
 Sbjct: 782 PSYDPDTRSS-CSSGDDSVFSPDPMPYEPCLPQYP 814

sp_vs P21802-18 Isoform 18 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens] 820 AA
FGFR2_HUMAN (Human)] align

Score = 1100 bits (2845), Expect = 0.0
Identities = 535/694 (77%), Positives = 604/694 (87%), Gaps = 9/694 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGGDDEDDTGAEDFVSENNSNNR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSPDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVERSPHRPILQAGLPAN + G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGDFEVCKVYSDAQPHIQWIKHVEKGNSKYG 302

Query: 211 PDNL PYVQILKHSGINSSDAEVLTLFNVTEAQS GEYVCKVSNYIGEANQSAWLT VTRPVA 270
PD LPY++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLT V P
Sbjct: 303 PDGL PYLKV LKHSGINSSNAEVLALFNVTEADAGEYI CKVSNYIGQANQSAWLT V -PKQ 361

Query: 271 KALEERPAVMSPLYLEIIYCTGAFLISCMILGSVIYKMKSGTKSDFHQSMAVHKLAK 330
+A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIAYCIGVFLIACMVVIVILCRMKNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSG-TPMLAGVSEYELPEDPRWELPRDR 388
IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQV--SAESSSSMNSNTPLVRITTRLSSADTPMLAGVSEYELPEDPKWEFPRDK 479

Query: 389 LVLGKPLGEGCFGQVVL AEAIGLDKDKNRVTKVAVKMLKSDATEKDLSLDL SEMEMMKM 448
L LGKPLGEGCFGQVVA+AEA+G+DKDP VAVKMLK DATEKDLSLDL+SEMEMMKM
Sbjct: 480 LTGKPLGEGCFGQVVM AEAVGIDKDPK EA VAVKMLKDDATEKDLSLDL SEMEMMKM 539

Query: 449 IGKHKNIINLLEACTQDGPLV VIVEYASKGNLREYLQARRPGLEYCYNPSHNPEEQQLSS 508
IGKHKNIINLL ACTQDGPLV VIVEYASKGNLREYL+ARRPG+EY Y+ + PEEQ++
Sbjct: 540 IGKHKNIINLLGACTQDGPLV VIVEYASKGNLREYLARRPGMEYSYDINRVEEQMTF 599

Query: 509 KDLVSCAYQVARGMEYLASKKCIH RDLAARNVLVTEDNV MKIADFG LARDI HHIDYYKKT 568
KDLVSC YO+ARGMEYLAS+KCIH RDLAARNVLVTE+NVMK IADFG LARDI++ IDYYKKT
Sbjct: 600 KDLVSC T YQ LARGMEYL ASQKCIH RDLAARNVLVTE NVMK IADFG LARDI INNIDYYKKT 659

Query: 569 TNGLRPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYGPVVEELFKLLKEGH 628
TNGLRPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYGPVVEELFKLLKEGH
Sbjct: 660 TNGLRPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYGPVVEELFKLLKEGH 719

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLD RIVALTSNQEYLDLSIPLDQYS 688
RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYS
Sbjct: 720 RMDK PANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLD RILTTNEEYLDLSQPL EQYS 779

Query: 689 PSFPDTRSSCTCSSGEDSVFSHEPLPEEPCLP RHP 722
PS+PDT RSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 780 PSYPDTRSS-CSSGDDSVFSPDPMPYEPCLPQYP 812

sp P21802 Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) 821 AA
FGFR2_HUMAN (FGFR-2) (Keratinocyte growth factor receptor 2) (CD332 align
antigen) [FGFR2] [Homo sapiens (Human)]

Score = 1065 bits (2755), Expect = 0.0
Identities = 519/696 (74%), Positives = 592/696 (85%), Gaps = 12/696 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGGDDEDDTGAEDFVSENNSNNR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSPDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVERSPHRPILQAGLPAN + G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGDFEVCKVYSDAQPHIQWIKHVEKGNSKYG 302

Query: 211 PDNL PYVQILKHSGINSSDAEVLTLF--NVT AEYVCKVSNYIGEANQSAWLT VTRP 268
PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLT V
Sbjct: 303 PDGL PYLKV LKHSGINSSNAEVLALFNVTEADAGEYI CKVSNYIGQANQSAWLT VLP A 362

Query: 269 VAKALEERPAVMSPLYLEIIYCTGAFLISCMILGSVIYKMKSGTKSDFHQSMAVHKL 328

+ E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
 Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTVILCRMNTTCKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMILAGVSEYELPEDPRWELPR 386
 K IPLRRQTVSA+SS+SMNS LVR +RLSS+ TPMILAGVSEYELPEDP+WE PR
 Sbjct: 419 TKRIPRQQTVSAESSSSMNSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEFPR 478

Query: 387 DRVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLSEMEMM 446
 D+L LGKPLGEGCFGQVVA+AEA+G+DKDKP VAVKMLK DATEKDLSLDLSEMEMM
 Sbjct: 479 DKLTGKPLGEGCFGQVVMFAEVGIDKDKPKPEAVTVAVKMLKDDATEKDLSLDLSEMEMM 538

Query: 447 KMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPNHNPSEEQL 506
 KMIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
 Sbjct: 539 KMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLRAARRPPGMESYDINRVPEEQM 598

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHDLAARNVLVTEEDNVMIKIADEGLARDIHIDYYK 566
 + KDLVSC YQ+ARGMEYLAS+KCIHDLAARNVLVTE+NVMKIADFGGLARDI++ IDYYK
 Sbjct: 599 TFKDLVSCTYQLARGMEYLASKCITHDLAARNVLVTEENNVMKIADFGGLARDINNIDYYK 658

Query: 567 KTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFGVLLWEIFTLGSPYPGVVEELFKLLKE 626
 KTTNGRLPVKWMAPAEALFDR+YTHQSDVWSFGVLLWEIFTLGSPYPG+PVEELFKLLKE
 Sbjct: 659 KTTNGRLPVKWMAPAEALFDRVYTHQSDVWSFGVLMWEIFTLGSPYPGIPVVEELFKLLKE 718

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+Q
 Sbjct: 719 GHRMDKPACTNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNEEYLDLSQPLEQ 778

Query: 687 YSPSPDPDTRSSTSCTSSGEDSVFSHEPLPEEPCLPRLHP 722
 YSPSP+PDTRSS CSSG+DSVFS +P+P EPCLP++P
 Sbjct: 777 YSPSPDPDTRS-CSSGDDSVFSPDPMPYEPCLPQYP 813

sp_vs P21802-5 Isoform 5 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens] 819 AA
 FGFR2_HUMAN (Human)

Score = 1057 bits (2733), Expect = 0.0
 Identities = 517/696 (74%), Positives = 590/696 (84%), Gaps = 14/696 (2%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPEWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISGGDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPNTLRLKGKEFKPDHRIGGYKVRATWSIIMDSVVPSDKGNYTCIVENEYGSINH 150
 G P PT+RWLKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVENEYGSINH 242

Query: 151 TYQLDWWERSPHRPILQAGLPAKNTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDWWERSPHRPILQAGLPAKNTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG
 Sbjct: 243 TYHLDWWERSPHRPILQAGLPAKNTVALGSNVEFMCKVYSDAQPQHQWLKHIEVNGSKIG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLF- -NVTDAQSGEYVCKVSNYIGEANQSAWLTTRP 268
 PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLT
 Sbjct: 303 PDGLPYLKVLAQVNNTTDKEIEEVLYIRNVTEDAGEYTCLAGNSIGISFHSAWLTLP 362

Query: 269 VAKALEERPAVMTSPLYLEIIIICTGAFLISCMGLSVIIYKMKSGTKSDFHQSMAVHKL 328
 + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
 Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTVILCRMNTTCKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMILAGVSEYELPEDPRWELPR 386
 K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMILAGVSEYELPEDP+WE PR
 Sbjct: 419 TKRIPRQQTVSAESSSSMNSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEFPR 478

Query: 387 DRVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLSEMEMM 446
 D+L LGKPLGEGCFGQVVA+AEA+G+DKDKP VAVKMLK DATEKDLSLDLSEMEMM
 Sbjct: 479 DKLTGKPLGEGCFGQVVMFAEVGIDKDKPKPEAVTVAVKMLKDDATEKDLSLDLSEMEMM 538

Query: 447 KMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPNHNPSEEQL 506
 KMIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
 Sbjct: 537 KMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLRAARRPPGMESYDINRVPEEQM 598

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHDLAARNVLVTEEDNVMIKIADEGLARDIHIDYYK 566
 + KDLVSC YQ+ARGMEYLAS+KCIHDLAARNVLVTE+NVMKIADFGGLARDI++ IDYYK
 Sbjct: 597 TFKDLVSCTYQLARGMEYLASKCITHDLAARNVLVTEENNVMKIADFGGLARDINNIDYYK 656

Query: 567 KTTNGRLPVKWMAPAEALFDRIYTHQSDVWSFGVLLWEIFTLGSPYPGVVEELFKLLKE 626
 KTTNGRLPVKWMAPAEALFDR+YTHQSDVWSFGVLLWEIFTLGSPYPG+PVEELFKLLKE
 Sbjct: 657 KTTNGRLPVKWMAPAEALFDRVYTHQSDVWSFGVLMWEIFTLGSPYPGIPVVEELFKLLKE 718

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+Q
 Sbjct: 717 GHRMDKPACTNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNEEYLDLSQPLEQ 776

Query: 687 YSPSPDPDTRSSTSCTSSGEDSVFSHEPLPEEPCLPRLHP 722
 YSPSP+PDTRSS CSSG+DSVFS +P+P EPCLP++P
 Sbjct: 777 YSPSPDPDTRS-CSSGDDSVFSPDPMPYEPCLPQYP 811

sp_vs P21802-16 Isoform 16 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 822 AA align
FGFR2_HUMAN (Human)]

Score = 1051 bits (2719), Expect = 0.0
Identities = 517/699 (73%), Positives = 590/699 (84%), Gaps = 17/699 (2%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVVKFKCPSS 90
DA+ S +D+DD D + E N K +APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGGDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPNTLRLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
G P PT+RWLKNKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTMRWLKNGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSDKGNYTCIVENEYGSINH 242

Query: 151 TYQLDVERSPHRPILQAGLPANKTVALGSNEFMCKVYSDPQPHIQOWLKHIEVNGSKIG 210
TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVERSPHRPILQAGLPANASTVVGGDEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPLYVQIILK---HSGINSSDAEVLTFL--NVTEAQSGEYVCKVSNYIGEANQSAWLT 265
PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLT
Sbjct: 303 PDGLPYVAKVLKVLKAAGVNTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLT 362

Query: 266 TRPVAKALEERPAVMTSPLYLEIIYCTGAFLISCLMGSVIIYKMKSGTKKSDFHSQMAV 325
+ E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TTK DF SQ AV
Sbjct: 363 LPAPGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMKNITKKPDFSSQAV 418

Query: 326 HKLAKSIPLRRQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWE 383
HKL K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE
Sbjct: 419 HKLTKRIPLRQV--SAESSSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWE 476

Query: 384 LPRDRVLVLCKPLGEFCFGQVVAEAIQLDKDKPNRVTKVAVKMLKSDATEKDLSLSEM 443
PRD+L LGKPLGEFCFGQVVAEAIQLDKDKPNRVTKVAVKMLKSDATEKDLSLSEM
Sbjct: 477 FPRDKLTLCKPLGEFCFGQVVAEAVGIDDKPKPEAVTVAKMLKDDATEKDLSLSEM 536

Query: 444 EMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCYNPSHNPE 503
EMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYL-ARRPPG+EY Y+ + PE
Sbjct: 537 EMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVE 596

Query: 504 EQLSSKDLVSCAYQVARGMEYLASKKCIHRLAARNVLVTEDNVMKIADFGLARDIHID 563
EQ++ KDLVSC YQ+ARGMEYLAS+KCIHRLAARNVLVTE+NVMKIADEFGLARDI++ID
Sbjct: 597 EQMTFKDLVSCTYQLARGMEYLASQKCIHRLAARNVLVTEENNVMKIADEFGLARDINNID 656

Query: 564 YYKKTTNGRLPVKMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVPEELFKL 623
YYKKTTNGRLPVKMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVPEELFKL
Sbjct: 657 YYKKTTNGRLPVKMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGVVPEELFKL 716

Query: 624 LKEGHRMDKPSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRLIVALTSNQBYLDLSIP 683
LKEGHRMDKPSNCNTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+BYLDLS P
Sbjct: 717 LKEGHRMDKPSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRLITLTNEEYLDLSQP 776

Query: 684 LDQYSPSPFPDTRSSTCSSGEDSVFSHEPPLBEEPCPLPRHP 722
L+QYSPSP+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 777 LEQYSPSPYDPTRSS-CSSGDDDSVFSQDPMPYEPCLPQYP 814

sp_vs P21802-20 Isoform 20 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 704 AA align
FGFR2_HUMAN (Human)]

Score = 1046 bits (2706), Expect = 0.0
Identities = 520/726 (71%), Positives = 593/726 (81%), Gaps = 34/726 (4%)

Query: 1 MWGWKCLLFWAVILVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNPV 60
M W + V+ ATL ARP+ +L E D T
Sbjct: 1 MVSWGRFICLVVVTMATLSLARPSFSVL-----DTTLEPEG 37

Query: 61 APYWTSPPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRLKNGKEFKPDHRIGGYKVRAYA 120
APYWT+ EKMEK+LHAVPAA TVKF+CP+ G P PT+RWLKNKGKEFK +HRIGGYKVR
Sbjct: 38 APYWTNTEKMEKLHAVPAANTVKFRCPAGGNPMPMTMRWLKNGKEFKQEHHRIGGYKVRNQ 97

Query: 121 TWSTIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGS 180
WS+IM+SVVPSDKGNYTC+VENEYGSINHTY LDVVERSPHRPILQAGLPAN + +G
Sbjct: 98 HWSLIMESVVPSPDKGNYTCVVENEYGSINHTYHLDVVERSPHRPILQAGLPANASTVVGG 157

Query: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPLYVQIILKHSGINSSDAEVLTFL--NV 238
+VEF+CKVYSD QPHIQW+KH+E NGSK GPD LPY++LK +G+N++D E+ L+ NV
Sbjct: 158 DVEFVCKVYSDAQPHIQWIKHVEKNGSKYCPDGLPYLKVLAAGVNTTDKEIEVLYIRNV 217

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIYCTGAFLI 298
T +GEY C N IG + SAWLT + E + SP YLEI IYC G FLI

Objct: 218 TPEDAGEYTCAGNSIGISFHSAWLTVLPAPGREKE---ITASPDYLEIAIYCIGVFLI 273
 Query: 299 SCMLGSVIIYKMKSGTKKSDFHQSMAVHKLAKSISPLRRQVTVSADSSASMNSGVLLVR-P 357
 +CM+ +VI+ +MK+ TKK DF SQ AVHKL K IPILRQV SA+SS+SMNS LVR
 Objct: 274 ACMVVTIVILCRMKNTTCKPDFSSQPAVHKLTKRIPRLRQV--SAESSSSMNSNTPLVRIT 331
 Query: 358 SRLSSSG-TPMLAGVSEYELPEDPRWELPRDRLVLGKPLGECCFGQVVLAEAIGLDKDKP 416
 +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L LGKPLGECCFGQV+AEA+G+DKDKP
 Objct: 332 TRLSSTADTPMLAGVSEYELPEDPKWEFPDRKLTGKPLGECCFGQVVMMAEVGIDKD KP 391
 Query: 417 NRVTKVAVKMLKSDATEKDLSLSDISEMEMMMKIGKHKNIINLLACTQDGPLYVIVEYAS 476
 VAVKMLK DATEKDLSLSD+SEMEMMMKIGKHKNIINLL ACTQDGPLYVIVEYAS
 Objct: 392 KEAVTVAVKMLKSDATEKDLSLSDVSEMEMMMKIGKHKNIINLLGACTQDGPLYVIVEYAS 451
 Query: 477 KGNLREYLQARRPPGLEYCYNPSHNPPEEQLSSKDLVSCAYQARGMEYLASKKCIIHRDLA 536
 KGNLREYL+ARRPPG+EY Y+ + PEEQ++ KDLVSC YQ+ARGMEYLAS+KCIHRDLA
 Objct: 452 KGNLREYLARRPPGMEYSYDINRVPEEQMTFKDLVSCTYQLARGMEYLASQKCIIHRDLA 511
 Query: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYYKKTINGRLPVKWMMAPEALFDRIYTHQSDVWS 596
 ARNVLVTE+NMVKIADFGGLARDI++IDYYKKTINGRLPVKWMMAPEALFDR+YTHQSDVWS
 Objct: 512 ARNVLVTEDNVMKIADFGGLARDINNIDYYKKTNGRLPVKWMMAPEALFDRVYTHQSDVWS 571
 Query: 597 FGVLWEIFTLGSPYPGPVVEELFKLLKEGHHRMDKPSNCTNELYMMMRDCWHAVPSQR P 656
 FGVL+WEIFTLGSPYPGP+PVEELFKLLKEGHHRMDKP+NCTNELYMMMRDCWHAVPSQR P
 Objct: 572 FGVLWEIFTLGSPYPGP+PVEELFKLLKEGHHRMDKPANCTNELYMMMRDCWHAVPSQR P 631
 Query: 657 TFKQLVEVLDRIVALTSNQEYLDSLISPLDQYSPSPFPDRSSTCSSGEDSVFSHEPLPEEP 716
 TFKQLVE LDRI+ LT+N+EYLDLS PL+QYSPS+PDT RSS CSSG+DSVFS +P+P EP
 Objct: 632 TFKQLVEDLDRILTLTTNEEYLDLSQPLEQYSPSPYDTRSS-CSSGDDSVFSPDPMPYEP 690
 Query: 717 CLPRHP 722
 CLP++P
 Objct: 691 CLPQYP 696

sp_vs P21802-7 Isoform 7 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens] 817 AA
 FGFR2_HUMAN (Human)] align

Score = 1040 bits (2688), Expect = 0.0
 Identities = 507/674 (75%), Positives = 571/674 (84%), Gaps = 6/674 (0%)
 Query: 31 DALPSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKPKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Objct: 126 DAISSGGDEDDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRC PAG 182
 Query: 91 GTPNPNTLRLKGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
 G B PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENBYGSINH
 Objct: 183 GNPMPTMRWLKGKEFKQEHRRIGGYKVRNQHWSLIMESVVPSDKGNYTCVENEYGSINH 242
 Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VFP+CKVYSD QPHIQW+KH+E NGSK G
 Objct: 243 TYQLDVVERSPHRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKIG 302
 Query: 211 PDNLPYVQIHLKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY++ +LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTVA P
 Objct: 303 PDGLPYLKVLKHSGINSSNAEVLALFNTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361
 Query: 271 KALEERPAVMTSPLYLEIIIYCTGAFLISCMILGSVIIYKMKSGTKKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Objct: 362 QAPGREKEITASPDYLEIAIYCIGVPLIACMVVTVIICRMKNTTCKPDFSSQPAVHKLT K 421
 Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSG-TPMLAGVSEYELPEDPRWELPRDR 388
 IPILRQVTVS A+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Objct: 422 RIPLRRQVTVSSESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPDRK 481
 Query: 389 LVLGKPLGECCFGQVVLAEAIQLDKPKNRVTKVAVKMLKSDATEKDLSLSDISEMEMMMK 448
 L LGKPLGECCFGQV+AEA+G+DKDKP VAVKMLK DATEKDLSLSD+SEMEMMMK
 Objct: 482 LTLGKPLGECCFGQVVMMAEVGIDKDPKPEAVTVAVKMLKDDATEKDLSLSDVSEMEMMMK 541
 Query: 449 IGKHKNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPPEEQLSS 508
 IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
 Objct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601
 Query: 509 KDLVSCAYQARGMEYLASKKCIIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYYKKT
 Objct: 602 KDLVSCTYQLARGMEYLASQKCIIHRDLAARNVLVTEENVMKIADFGGLARDINNIDYYKKT 661
 Query: 569 TNGLRPVKWMAPEALFDRIYTHQSDWVSGVLLWEIFTLGSPYPGPVVEELFKLLKEGH 628
 TNGLRPVKWMAPEALFDR+YTHQSDWVSGVLL+WEIFTLGSPYPGP+PVEELFKLLKEGH
 Objct: 662 TNGLRPVKWMAPEALFDRVYTHQSDWVSGVLLWEIFTLGSPYPGP+PVEELFKLLKEGH 721
 Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQBYLDLSIPLDQYS 688
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ Y L P
 Objct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNERYKLLPCPDHNK 781

Query: 689 PSFPDTRSSTCSSL 702
 P+ R +G
 Sbjct: 782 RCKPEERGDLTEAG 795

sp_vs P21802-9 Isoform 9 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA align
 FGFR2_HUMAN (Human)]

Score = 1036 bits (2680), Expect = 0.0
 Identities = 503/653 (77%), Positives = 566/653 (86%), Gaps = 6/653 (0%)

Query: 31 DALPSSEDDDDDSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFCKPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGDDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKNGKEFKQEHRRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGGDVFVCKVYSDAQPHIQWLKHIEVNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY++LKHSGINSS+AELV LFNTEA +GEY+CKVSNYIG+ANQSAWLTVA
 Sbjct: 303 PDGLPYLKVLCVHSQNSNAEVLAFLNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAMVTSPLYLEIIYCTGAFLISCMILGSVIYKMKSGTKKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTIVLCRMKNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVVR-PSRLSSG-TPMLAGVSEYELPEDPRWEPLRDR 388
 SIPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSASESSSMSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEPLRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAIQLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMMKM 448
 L LGKPLGEGCFGQVVA+AEA+G+DKDP VAVKMLK DATEKDLSLDL+SEMEMMKM
 Sbjct: 482 LTGKPLGEGCFGQVMAEAVGIDDKDPKEAVTVAVKMLKSDATEKDLSLDL+SEMEMMKM 541

Query: 449 IGKHKNIIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNQSHNPEEQLSS 508
 IGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPG+EY Y+ + PEEQ++
 Sbjct: 542 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLARRRPGMMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQARGMYEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI+IDYYKKT
 Sbjct: 602 KDLVSCTYQLARGMEYLASQKCIHRDLAARNVLVTENNNVMKIADFGGLARDINNIDYYKKT 661

Query: 569 TNGLRPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKEGH 628
 TNGLRPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKEGH
 Sbjct: 662 TNGLRPVKWMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLS 681
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ L L+
 Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNERILTLT 774

sp_vs P21802-10 Isoform 10 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA align
 FGFR2_HUMAN (Human)]

Score = 1035 bits (2676), Expect = 0.0
 Identities = 501/649 (77%), Positives = 564/649 (86%), Gaps = 6/649 (0%)

Query: 31 DALPSSEDDDDDSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFCKPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGDDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKNGKEFKQEHRRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGGDVFVCKVYSDAQPHIQWLKHIEVNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY++LKHSGINSS+AELV LFNTEA +GEY+CKVSNYIG+ANQSAWLTVA
 Sbjct: 303 PDGLPYLKVLCVHSQNSNAEVLAFLNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAMVTSPLYLEIIYCTGAFLISCMILGSVIYKMKSGTKKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTIVLCRMKNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR -PSRLSSSG -TPMLAGVSEYELPEDPRWELPRDR 388
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDPKNRVTKVAVKMLKSDATEKDLSLDLISEMEMMMK 448
 L LGKPLGEGCFGQVVA+AEA+G+DKDKP VAVKMLK DATEKDLSLDL+SEMEMMMK
 Sbjct: 482 LTIGKPLGEGCFGQVVMMAEVGIDKDKPKEAVTVAVKMLKDATEKDLSLDLVESEMEMMMK 541

Query: 449 IGHKHNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSS 508
 IGHKHNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
 Sbjct: 542 IGHKHNIIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIIHDLAARNVLVTTE+NVMKIADFGLARDI++IDYYKKT
 Sbjct: 602 KDLVSCTYQLARGMEYLASKKCIIHDLAARNVLVTENNVMKIADFGLARDINNIDYYKKT 661

Query: 569 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKEGH 628
 TNGRLPVWKWMAPEALFDR+YTHQSDVWSFGVLL+WEIFTLGGSPYPG+PVEELFKLLKEGH
 Sbjct: 662 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVPEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDIVALTSNQ 675
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ +
 Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNEF 770

sp_vs P21802-11 Isoform 11 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 830 AA align
 FGFR2_HUMAN (Human)]

Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVPAPYWTSPKMEKKLHAVPAAKTVFKFCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISGGDDEDDTGAEDFVSESENSNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPNTLRLKGKEFKPDHRIGGYKVRATWSIIMDSVPSDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNGKEFK+HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKGKEFKQEHRIGGYKVRNQHWSLIMESVVPDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEP+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANSQAWLTIVTRPVA 270
 PD LPY+++-LKHSGINSS-AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTIV P
 Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLAFLFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAPVMTSPLYLEIYCTGAFLISCMILGSVIIYKMKSGTKKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITAASPDLYEIAIYCIGVFLIACMVVTVILCRMKNITKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR -PSRLSSSG -TPMLAGVSEYELPEDPRWELPRDR 388
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDPKNRVTKVAVKMLKSDATEKDLSLDLISEMEMMMK 448
 L LGKPLGEGCFGQVVA+AEA+G+DKDKP VAVKMLK DATEKDLSLDL+SEMEMMMK
 Sbjct: 482 LTIGKPLGEGCFGQVVMMAEVGIDKDKPKEAVTVAVKMLKDATEKDLSLDLVESEMEMMMK 541

Query: 449 IGHKHNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSS 508
 IGHKHNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
 Sbjct: 542 IGHKHNIIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIIHDLAARNVLVTTE+NVMKIADFGLARDI++IDYYKKT
 Sbjct: 602 KDLVSCTYQLARGMEYLASKKCIIHDLAARNVLVTENNVMKIADFGLARDINNIDYYKKT 661

Query: 569 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKEGH 628
 TNGRLPVWKWMAPEALFDR+YTHQSDVWSFGVLL+WEIFTLGGSPYPG+PVEELFKLLKEGH
 Sbjct: 662 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVPEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDIVALTSNQ 675
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ +
 Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNE 768

sp_vs P21802-12 Isoform 12 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 771 AA align
 FGFR2_HUMAN (Human)]

Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAAPYWTSPEKMEKKLHAVPAAKTVFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGGDEDDDTDGAEDFVSESNNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPRTLWLNKGKEFKPDHRIGGYKVRATWSIIMDSVVPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKNKGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSDKGNYTCIVENEYGSINH 242

Query: 151 TYQLDVVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQIHLKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY++LKHSGINSS+AELV LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
 Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLAFLPNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIYKMKSGTKKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVTILCRMNKNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSADTPMLAGVSEYELPEDPKWEFPDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEALDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMMMKM 448
 L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSLDL+SEMEMMMKM 541
 Sbjct: 482 LTLGKPLGEGCFGQVVMMAEVGIDKDKPKEAVTVAVKMLKDDATEKDLSLDLVESEMEMMMKM 541

Query: 449 IGKHKNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSS 508
 IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
 Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMELYASKKCIIHDLAARNVLVTEDNVMIKIADEFGLARDIHHIDYYKKT 568
 KDLVSC YQ+ARGMELYAS+KCIIHDLAARNVLVTE+NVMKIADFGLARDI++IDYYKKT
 Sbjct: 602 KDLVSCTYQLARGMELYASQKCIIHDLAARNVLVTENNVMKIADFGLARDINNIDYYKKT 661

Query: 569 TNCRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEITLGGSPYPGVVEELFKLLKEGH 628
 TNCRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEITLGGSPYPG+VEELFKLLKEGH
 Sbjct: 662 TNCRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEITLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
 Sbjct: 722 RMDK PANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNE 768

sp_vs_P21802-13 Isoform 13 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens] 768 AA align
 FGFR2_HUMAN (Human)

Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAAPYWTSPEKMEKKLHAVPAAKTVFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGGDEDDDTDGAEDFVSESNNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPRTLWLNKGKEFKPDHRIGGYKVRATWSIIMDSVVPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKNKGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSDKGNYTCIVENEYGSINH 242

Query: 151 TYQLDVVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQIHLKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY++LKHSGINSS+AELV LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
 Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLAFLPNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIYKMKSGTKKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVTILCRMNKNTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSADTPMLAGVSEYELPEDPKWEFPDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEALDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMMMKM 448
 L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSLDL+SEMEMMMKM 541
 Sbjct: 482 LTLGKPLGEGCFGQVVMMAEVGIDKDKPKEAVTVAVKMLKDDATEKDLSLDLVESEMEMMMKM 541

Query: 449 IGKHKNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSS 508
 IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++

Subject: 542 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601
 Query: 509 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGGLARDIHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIIHDLAARNVLVTE+NVMKIADEFGGLARDI++ IDYYKKT
 Subject: 602 KDLVSCTYQLARGMEYLASKKCIIHDLAARNVLVTENNVMKIADFGGLARDINNIDYYKKT 661
 Query: 569 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGH
 Subject: 662 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVVEELFKLLKEGH 721
 Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
 Subject: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNE 768

sp_vs P21802-17 Isoform 17 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 769 AA align
 FGFR2_HUMAN (Human)]

Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)
 Query: 31 DALPSSSEDDDDDDSSSEEKETDNTPKPNPVAHYWTSPKEMKKLHAVPAAKTVFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Subject: 126 DAISSGDDEDDTDGAEDFVSENSNNKRR--APYWTNTKEKMEKRLHAVPAANTVKFRCPAG 182
 Query: 91 GTPNPRTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Subject: 183 GNMPMPTMRWLKNGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSINH 242
 Query: 151 TYQLDGVVERSPHRPILOAGLPANKTVALGSNVEMCKVYSDPQPHIQOWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILOAGLPAN + +G +VEF+CKVYSD QPHIOW+KH+E NGSK G
 Subject: 243 TYHLDGVVERSPHRPILOAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302
 Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY+++LKHSGINSS+AEVL +GEY+CKVSNYIG+ANQSAWLTV P
 Subject: 303 PDGLPYLKVILKHSGINSSNAEVLAFLFNVTEADAGEYICKVSNSYIGQANQSAWLTVL-PKQ 361
 Query: 271 KALEERPAVMTSPLYLEI IIYCTGAFLISCMGLSVIIYKMKSGTKSDFHQSMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ T KK DF SQ AVHKL K
 Subject: 362 QAPGREKEITASPDLYEIAIAYCIGVFLIACMVVTILCRMKNTKPDFSSQPAVHKLTK 421
 Query: 331 SIPLRRQTVVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
 IPIPLRRQTVVSA-SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Subject: 422 RIPLRRQTVVSAESSSMSNTPLVIRITTRLSTATDPMLAGVSEYELPEDPKWEFPRDK 481
 Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKAVAKMLKSDATEKDLSLDLISEMEMMKM 448
 L LGKPLGEGCFGQVV+AEE+G+DKDP VAVKMLK DATEKDLSLD+SEMEMMKM
 Subject: 482 LTLGKPLGEGCFGQVVMMAEVGIDKDPKPEAVTVAVKMLKDDATEKDLSLDLVSEMEMMKM 541
 Query: 449 IGKHKNIIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
 IGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL-AARRPPG+EY Y+ + PEEQ++
 Subject: 542 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTF 601
 Query: 509 KDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGGLARDIHIDYYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIIHDLAARNVLVTE+NVMKIADEFGGLARDI++ IDYYKKT
 Subject: 602 KDLVSCTYQLARGMEYLASKKCIIHDLAARNVLVTENNVMKIADFGGLARDINNIDYYKKT 661
 Query: 569 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGH
 Subject: 662 TNGRLPVWKWMAPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVVEELFKLLKEGH 721
 Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
 Subject: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNE 768

sp_vs P21802-4 Isoform 4 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 682 AA align
 FGFR2_HUMAN (Human)]

Score = 1029 bits (2661), Expect = 0.0
 Identities = 507/676 (75%), Positives = 570/676 (84%), Gaps = 14/676 (2%)
 Query: 1 MWGWKCLLFWAVLVTATLCTARPA-----PTLPEQDALPSSEDDDDDDSSSEEKETDN 54
 M W + V+ ATL ARP+ TL +DA+ S +D+DD D + E N
 Subject: 1 MVSWGRFICLUVVTMATLSLARPSFLVEDTLEPEDAISSGDDEDDTDGAEDFVSESN 60
 Query: 55 TKPNPVAHYWTSPKEMKKLHAVPAAKTVFKCPSSGTPNPTLRLKNGKEFKPDHRIGG 114
 K APYWT+ EKMEK+LHAVPAA TVKF+CP+ G P PT+RWLKNGKEFK +HRIGG
 Subject: 61 NKR--APYWTNTKEKMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHHRIGG 117
 Query: 115 YKVRVYATWSIIMDSVVPDKGNYTCIVENEYGSINHTYQLDGVVERSPHRPILOAGLPANK 174

YKVR WS+IM+SVVPSDKGNYTC+VENEYGSINHTY LDVVERSPHRPIIQLQAGLPAN
 Sbjct: 118 YKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSINHTYHLDVVERSPHRPIIQLQAGLPANA 177

Query: 175 TVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKHSGINSSDAEVLT 234
 + G +VEF+CKVYSD QPHIQW+KH+E NGSK GPD LPY+++LKHSGINSS+AEVL
 Sbjct: 178 STVVGGDVEFVCKVYSDAQPHIQWLKHVEKNGSKYGPDGLPYLKVLKHSGINSSNAEVL 237

Query: 235 LFNVTTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIIYCTG 294
 LFNVTTEA +GEY+CKVSNYIG+ANQSAWLTVP +A + SP YLEI IYC G
 Sbjct: 238 LFNVTTEADAGEYICKVSNYIGQANQSAWLTVL-PKQQAPGREKEITASPDYLEIAIYCG 296

Query: 295 AFLISCMGLGSVIIYKMKSGTKKSDFHQSMAVHKLAKSIPLRROQTVSADSSASMNSGVLL 354
 FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K IPLRQV SA+SS+SMNS L
 Sbjct: 297 VFLIACMVVTIVLCRMKNNTKKFDSSQPAVHKLTKRIPRQV-SAESSSSMNSNTPL 354

Query: 355 VR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDRVLVGLKPLGEGCFGQVVAEEAIGLD 412
 VR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L LGKPLGEGCFGQVVAEEA+G+D
 Sbjct: 355 VRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPRDKLTLGKPLGEGCFGQVVAEEAVGID 414

Query: 413 KDPNVRTKVAVKMLKSDATEKDLSDLISEMEMMMKMGKHKNIINLLEACTQDGPLYVIV 472
 KDPK VAVKMLK DATEKDLSDL+SEMEMMMKMGKHKNIINLLEACTQDGPLYVIV
 Sbjct: 415 KDPKPEAVTVAVKMLKSDATEKDLSDLVSEMEMMMKMGKHKNIINLLEACTQDGPLYVIV 474

Query: 473 EYASKGNLREYLQARRPPGLEYCYNPNSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIH 532
 EYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++ KDLVSC YQ+ARGMEYLAS+KCIH
 Sbjct: 475 EYASKGNLREYLARRPPGMEYSYDINRVPEBQMTFKDLVSCTYQLARGMEYLASKKCIH 534

Query: 533 RDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPPEALFDRYTHQS 592
 RDLAARNVLVTTE+NVMKIADEFGLARDI++IDYYKKTTNGRLPVKWMAPPEALFDR+YTHQS
 Sbjct: 535 RDLAARNVLVTENNVMKIADEFGLARDINNIDYYKKTTNGRLPVKWMAPPEALFDRYTHQS 594

Query: 593 DVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVP 652
 DVWSFGVLL+WEIFTLGGSPYPGP+PVEELFKLLKEGHRMDK+P+CTNELYMMMRDCWHAVP
 Sbjct: 595 DVWSFGVLMWEIFTLGGSPYPGPVVEELFKLLKEGHRMDKPCNACTNELYMMMRDCWHAVP 654

Query: 653 SQRPTFKQLVEVLDR 668
 SQRPTFKQLVE LDRI
 Sbjct: 655 SQRPTFKQLVEDLDRI 670

tr Q1KHYS Fibroblast growth factor receptor 2 (Bacteria-expressed kinase, 785 AA
 Q1KHYS_HUMAN keratinocyte growth factor receptor, craniofacial align
 dysostosis 1, Crouzon syndrome, Pfeiffer syndrome,
 Jackson-Weiss syndrome) [FGFR2] [Homo sapiens (Human)]

Score = 1011 bits (2615), Expect = 0.0
 Identities = 495/669 (73%), Positives = 563/669 (84%), Gaps = 13/669 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVFKFCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGDDDEDDTDGAEDFVSENSNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCAG 182

Query: 91 GTPNPTLRLKNGKEFKPDKPHIRIGGYKVRATWSIIMDSVVPDSKGNYTCIVENEYGSINH 150
 G P PT+RWLKGNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMWRWLKGKEFKQEHIRIGGYKVRNQHWSLIMESVVPSDKGNYTCIVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPIQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPIQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPHRPIQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWLKHVEKNGSKYG 302

Query: 211 PDNLPLYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
 PD LPY++L+K +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
 Sbjct: 303 PDGLPYLKVLKAQVNNTTDKEIEVLYIRNVTEDAGEYTCAGNSIGISFHSAWLTVLPA 362

Query: 269 VAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMGLGSVIIYKMKSGTKKSDFHQSMAVHKL 328
 + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
 Sbjct: 363 PGREKE---ITASPDYLEIAIYICIGVFLIACMVVTIVLCRMKNNTKKFDSSQPAVHKL 418

Query: 329 AKS1PLRROQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
 K IPLRROQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
 Sbjct: 419 TKRIPRQV--SAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
 D+L LGKPLGEGCFGQVVAEEA+G+DKDP VAVKMLK DATEKDLSDL+SEMEMM
 Sbjct: 477 DKLTLGKPLGEGCFGQVVMAEAVGIDDKPKPEAVTVAVKMLKDDATEKDLSDLVSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPNSHNPEEQL 506
 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
 Sbjct: 537 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRLAARNVLVTEDNVMKIADFGLARDIHHIDYYK 566
 + KDLVSC YQ+ARGMEYLAS+KCIHRLAARNVLVTE+NVMKIADEFGLARDI++IDYYK
 Sbjct: 597 TFKDLVSCTYQLARGMEYLASQKCIHRLAARNVLVTEENNVMKIADEFGLARDINNIDYYK 656

Query: 567 KTTNGRLPVKWMAPPEALFDRYTHQSDFVWSFGVLLWEIFTLGGSPYPGPVVEELFKLL 626

KTTNGRLPVKWMMAPEALFDR+YTHQSDVWSFGV+WEIFTLGGSPYPG+PVEELFKLLKE
 Sbjct: 657 KTTNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+
 Sbjct: 717 GHRMDKPACTNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEP 776

Query: 687 YSPSFDPTR 695
 YSP +PD R
 Sbjct: 777 YSPCYPDPR 785

sp_vs P21802-6 Isoform 6 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 785 AA align
 FGFR2_HUMAN (Human)]

Score = 1011 bits (2615), Expect = 0.0
 Identities = 495/669 (73%), Positives = 563/669 (84%), Gaps = 13/669 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
 DA+ S +D+D D + E N K APYWT+ EKMEK-LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGDDEDDTGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPNTLRLKGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRLKGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDGVVERSPHRPILQAGLPANKTVALGSNVEMCCKVYSDPQPHIQWKLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDGVVERSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPLYVQILKHSGINSSDAEVLTLE--NVTFAQSGEVVCKVSNYIGEANQSAWLTVTRP 268
 PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
 Sbjct: 303 PDGLPYLKLKAAGVNNTDKIEIVLYIRNVTIEDAGEYTCLAGNSIGISPHSAWLTVLPA 362

Query: 269 VAKALEERPAVMTSPLYLEIIYCTGAFLISCMGLGSVIIYKMKSGTKSDPHSQMAVHKL 328
 + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
 Sbjct: 363 PGREKE----ITASPDLYEIAIYCIGVFLIACMVVTILCRMKNNTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRQQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
 K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
 Sbjct: 419 TKRIPRQQV--SAEASSSMSNTPLVRITTRLSTATDTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMM 446
 D+L LGKPLGEGCFGQV+AEA+G+DKDP VAVKMLK DATEKDLSLDL+SEMENN
 Sbjct: 477 DKLTLGKPLGEGCFGQVVMMEA VAVGIDKDKPKAEVTVAVKMLKDDATEKDLSLDL+SEMENN 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPSEEQL 506
 KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
 Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKC1HRDLAARNVLVTEDNVMIADFGLARDIHHDYYK 566
 + KDLVSC YQ+ARGMEYLAS+KC1HRDLAARNVLVTE+NVMIADFGLARDI++IDYYK
 Sbjct: 597 TFKDLVSCTYQLARGMEYLASKKC1HRDLAARNVLVTEENNVMKIADFGLARDINNIDYYK 656

Query: 567 KTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELPKLLKE 626
 KTTNGRLPVKWMMAPEALFDR+YTHQSDVWSFGV+WEIFTLGGSPYPG+PVEELFKLLKE
 Sbjct: 657 KTTNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+
 Sbjct: 717 GHRMDKPACTNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEP 776

Query: 687 YSPSFDPTR 695
 YSP +PD R
 Sbjct: 777 YSPCYPDPR 785

sp_vs P11362-10 Isoform 7 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 573 AA align
 FGFR1_HUMAN (Human)]

Score = 998 bits (2579), Expect = 0.0
 Identities = 496/533 (93%), Positives = 508/533 (95%), Gaps = 8/533 (1%)

Query: 1 MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPN-- 58
 MW WKCLLFWAVLVTATLCTARP+PTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPN
 Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSTLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNRM 60

Query: 59 PVAPYWTSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
 PVAPYWTSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
 Sbjct: 61 PVAPYWTSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILOAGLPANKTVAL 178
 YATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILOAGLPANKTVAL 180
 Sbjct: 121 YATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILOAGLPANKTVAL 180
 Query: 179 GSNVEFMCKVYSDPOPHIQWLKHIEVNNGSKIGPDNLPYVQILKHSGINSSDAE--VLTLF 236
 GSNVEFMCKVYSDPQPHIQWLKHIEVNNGSKIGPDNLPYVQILK +G+N++D E VL L
 Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNNGSKIGPDNLPYVQILKTAGVNNTDKEMEVHLR 240
 Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTTRPAKALEERPAVMTSPLYLEIIIIYCTGAF 296
 NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAF
 Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAF 296
 Query: 297 LISCMMLGSVIIYMKMKGKSDFHQSMAVHKLAKSIPLRROQTVSADSSASMNSGVLLVR 356
 LISCM:GSVII+YMKMKGKSDFHQSMAVHKLAKSIPLRROQTVSADSSASMNSGVLLVR
 Sbjct: 297 LISCMVGSVIVYMKMKGKSDFHQSMAVHKLAKSIPLRROQTVSADSSASMNSGVLLVR 356
 Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDWP 416
 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDWP
 Sbjct: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDWP 416
 Query: 417 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLACTQDGPLYVIVEYAS 476
 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLACTQDGPLYVIVEYAS
 Sbjct: 417 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLGACTQDGPLYVIVEYAS 476
 Query: 477 KGNLREYLQARRPPGLEYCYNPSHNPSEEQLSSKDLVSCAYQVARGMEYLASKK 529
 KGNLREYLQARRPPGLEYCYNPSHNPSEEQLSSKDLVSCAYQVARGMEYLASKK
 Sbjct: 477 KGNLREYLQARRPPGLEYCYNPSHNPSEEQLSSKDLVSCAYQVARGMEYLASKK 529

sp_vs P21802-2 Isoform 2 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 768 AA
 FGFR2_HUMAN (Human)] align

Score = 991 bits (2561), Expect = 0.0
 Identities = 483/649 (74%), Positives = 549/649 (84%), Gaps = 11/649 (1%)
 Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVKFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ BKMEK+LHAVPAA TVKP+CP+
 Sbjct: 126 DAISSGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182
 Query: 91 GTPNPNTLRLKGKEFKPDHRIGGYKVRATWSIIMDSVVPSDKGNYTCIVENEYGSINH 150
 G P PT+RWLKGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKGKEFKQEHRRIGGYKVRNQHWSLIMESVVPSPDKGNYTCVENEYGSINH 242
 Query: 151 TYQLDVVERSPHRPILOAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNNGSKIG 210
 TY LDVVERSPHRPILOAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPHRPILOAGLPANASTVVGGDVEFVCKVYSDAQPHIQWLKHVEKNGSKYG 302
 Query: 211 PDNLPYVQILKHSGINSSDAEVLTFL--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTTRP 268
 PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
 Sbjct: 303 PDGLPYLKVLAQVNTTDKEIEVLYIRNVTEDAGEYTCLAGNSIGISFHSAWLTVLPA 362
 Query: 269 VAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMGLGSVIIYMKMKGKSDFHQSMAVHKL 328
 + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
 Sbjct: 363 PGREKE---ITASPDYLEIAIYICVFLIACMVVTILCRMNTTKPDFSSQPAVHKL 418
 Query: 329 AKSIPLRROQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
 K IPLLRRQVTVA-SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
 Sbjct: 419 TKRIPLRRQVTVAESSSSMSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEFPR 478
 Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRVTKVAVKMLKSDATEKDLSLDISEMEMM 446
 D+L LGKPLGEGCFGQVVLAEA+G+DKDP VAVKMLK DATEKDLSLD+SEMEMM
 Sbjct: 479 DKLTLGKPLGEGCFGQVVMMEAAGVIDDKDPKEAVTVAVKMLKDDATEKDLSLDVSEMEMM 538
 Query: 447 KMIGKHKNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPSEEQL 506
 KMIGKHKNIINLLACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
 Sbjct: 539 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRRPPGMEYSYDINRVPEEQM 598
 Query: 507 SSKDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHIDYYK 566
 + KDLVSC YQ+ARGMEYLAS+KCIHDLAARNVLVTE+NVMKIADFGLARDI++IDYYK
 Sbjct: 599 TFKDLVSCTYQIARGMEYLASKCIIHDLAARNVLVTEENNVMKIADFGLARDINIDYYK 658
 Query: 567 KTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE 626
 KTTNGRLPVKWMAPEALFD+YTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKE
 Sbjct: 659 KTTNGRLPVKWMAPEALFDRTVTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 718
 Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
 Sbjct: 719 GHRMDKPACTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTTNE 767

sp_vs P11362-11 Isoform 9 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 571 AA
 FGFR1_HUMAN (Human)] align

Score = 989 bits (2557), Expect = 0.0
 Identities = 494/533 (92%), Positives = 506/533 (94%), Gaps = 10/533 (1%)

Query: 1 MWGKWLFWAVLVTATLCTARPAPTLPEQDALPSSEDDDDDSSEEKETDNTKPN-- 58
 MW WKCLLFWAVLVTATLCTARP+PTLPEQDALPSSEDDDDDSSEEKETDNTKPN
 Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSTPLPEQDALPSSEDDDDDSSEEKETDNTKPNRM 60

Query: 59 PVAPYWTSPPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
 PVAPYWTSPPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
 Sbjct: 61 PVAPYWTSPPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVAL 178
 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVAL
 Sbjct: 121 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAE--VLTLF 236
 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILK +G-N++D E VL L
 Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNNTDKEMEVHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTTRPAKALEERPAVMTSPLYLEIIYCTGAF 296
 NV+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIYCTGAF
 Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSawLTV---EALEERPAVMTSPLYLEIIYCTGAF 296

Query: 297 LISCMGLSVIYKMKSGTKKSDFHSMQAVHKLAKSIPLRQVTSADSSASMNSGVLLVR 356
 LISCM+GSVI+YKMKSGTKKSDFHSMQAVHKLAKSIPLRQV SADSSASMNSGVLLVR
 Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSMQAVHKLAKSIPLRQV--SADSSASMNSGVLLVR 354

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCCPGQVVLAEAIGLDKDP 416
 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCCPGQVVLAEAIGLDKDP
 Sbjct: 355 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCCPGQVVLAEAIGLDKDP 414

Query: 417 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLLEACTQDGPLYVIVEYAS 476
 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLL ACTQDGPLYVIVEYAS
 Sbjct: 415 NRVTKVAVKMLKSDATEKDLSLDISEMEMMMKIGKHKNIINLGACTQDGPLYVIVEYAS 474

Query: 477 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKK 529
 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKK
 Sbjct: 475 KGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKK 527

sp_vs P21802-8 Isoform 8 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 766 AA align
 FGFR2_HUMAN (Human)]

Score = 982 bits (2539), Expect = 0.0
 Identities = 481/649 (74%), Positives = 547/649 (84%), Gaps = 13/649 (2%)

Query: 31 DALPSSSEDDDDDSSEEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISSGGDEDDETDGAEDFVSESNNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPNTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
 G P PT+RWLKGNGKEFK +HRIGGYKVR WS+IM-SVVPSPDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPTMRWLKNGKEFKQEHHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGSNEFMCVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPHRPILQAGLPAN +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPHRPILQAGLPANASTVVGDFEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTFLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTTRP 268
 PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
 Sbjct: 303 PDGLPYLKVLAAGVNNTDKEIEVLYIRNVTEDAGEYTCLAGNSIGISFHSAWLTLP 362

Query: 269 VAKALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIYKMKSGTKKSDFHSMQAVHKL 328
 + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
 Sbjct: 363 PGREKE---ITASPDLYEIAIYCIGVFLIACMVVTILCRMNTTKEFDSSQPAVHKL 418

Query: 329 AKSIPLRQRQTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
 K IPLRQRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPED+WE PR
 Sbjct: 419 TKRIPLRRQV--SAESSSSMNSNTPLVRITTRLSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRDVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKAVKMLKSDATEKDLSLDISEMEMM 446
 D+L LGKPLGEGCFGQVV+AEA+G+DKDP VAVKMLK DATEKDLSLD+SEMEMM
 Sbjct: 477 DKLTLGKPLGEGCFGQVVMEEAVGIDKDKPKEAVTVAVKMLKDATEKDLSLDLVESEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQL 506
 KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
 Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIHIDYYK 566
 + KDLVSC YQ+ARGMEYLAS+KCIHDLAARNVLVTE+NVMKIADEGLARDI++IDYYK
 Sbjct: 597 TFKDLVSCTYQLARGMEYLASQKCIHDLAARNVLVTENNVMKIADEGLARDINIDYYK 656

Query: 567 KTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVVEELFKLLKE 626
 KTNGRLPVKWMMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKE

Sbjct: 657 KTTNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVBEELFKLLKE 716
 Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
 Sbjct: 717 GHRMDK PANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNE 765

sp_vs P11362-8 Isoform 2 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 662 AA align
 FGFR1_HUMAN (Human)]

Score = 934 bits (2415), Expect = 0.0
 Identities = 468/503 (93%), Positives = 479/503 (95%), Gaps = 8/503 (1%)

Query: 31 DALPSSSEDDDDDDDSSEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVFKCP 88
 DALPSSSEDDDDDDDSSEEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVFKCP
 Sbjct: 120 DALPSSSEDDDDDDDSSEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVFKCP 179

Query: 89 SSGTPNPTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGS 148
 SSGTPNPTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGS
 Sbjct: 180 SSGTPNPTLRLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGS 239

Query: 149 NHTYQLDVERSPHRPILOQALPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
 NHTYQLDVERSPHRPILOQALPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVERSPHRPILOQALPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDNLPVQI LKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
 IGPDNLPVQI LK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLT
 Sbjct: 300 IGPDNLPVQI LKTAGVN TTDKEMEMEVHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLT 359

Query: 267 RPVAKALEERPAVMSPPLYLEIIIIYCTGAFLISCMGLSVIYKMKSGTKKSDFHQSMAVH 326
 +ALEERPAVMSPPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHQSMAVH
 Sbjct: 360 ---EALEERPAVMSPPLYLEIIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHQSMAVH 415

Query: 327 KLAKS1PLRRQVTVSADSSASMNSGVLLVRPSSLSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAKS1PLRRQVTVSADSSASMNSGVLLVRPSSLSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAKS1PLRRQVTVSADSSASMNSGVLLVRPSSLSSGTPMLAGVSEYELPEDPRWELPR 475

Query: 387 DRLVLGKPLGEGCFGQVVLAEAI GLDKDKPNRVTKVAVKMLKSDATEKDLSLDI SEMMM 446
 DRLVLGKPLGEGCFGQVVLAEAI GLDKDKPNRVTKVAVKMLKSDATEKDLSLDI SEMMM
 Sbjct: 476 DRLVLGKPLGEGCFGQVVLAEAI GLDKDKPNRVTKVAVKMLKSDATEKDLSLDI SEMMM 535

Query: 447 KMIGKHKNIIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQL 506
 KMIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQL
 Sbjct: 536 KMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQL 595

Query: 507 SSKDLVSCAYQVARGMEYLASKK 529
 SSKDLVSCAYQVARGMEYLASKK
 Sbjct: 596 SSKDLVSCAYQVARGMEYLASKK 618

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAFLVLTATLCTARPATPLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNPV 60
 MW WKCLLFWAFLVLTATLCTARP+PTLPEQ
 Sbjct: 1 MWSWKCLLFWAFLVLTATLCTARPSTPLPEQ----- 30

Query: 61 APYWTSPEKMEKKLHAVPAAKTVFKCPSSGTNPNTLRLKNGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL+G + +R R
 Sbjct: 31 AQPWGAPVEVESFL---VHPGDLLQLRCRLRDDVQ-SINWLRDGQVLAESNR----TRIT 82

Query: 121 TW SIIIMDSVVPDKGNYTCIVENEYGSINHTYQLDVVERSP----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVDALPSSSEDDDDDDSSSEEKETD 142

Query: 162 ----HRPILQAGLPANK-----TVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 P+ K V V-F C P P ++WLK NG +
 Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVFKCPSSGTNPNTLRLWLK---NGKEFK 198

Query: 211 PDNL PYVQILKHSGINSSDAEVLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVT--- 266
 PD+ +++ + + + +V + G Y C V N G N + L V
 Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVPDKGNYTCIVENEYGSINHTYQLDVVERSP 252

Query: 267 -RPVAKA 272
 RP+ +A
 Sbjct: 253 HRPILQA 259

sp_P22607 Fibroblast growth factor receptor 3 precursor (EC 2.7.10.1) 806 AA
 FGFR3_HUMAN (FGFR-3) (CD333 antigen) [FGFR3] [Homo sapiens (Human)] align

Score = 931 bits (2406), Expect = 0.0
 Identities = 462/685 (67%), Positives = 552/685 (80%), Gaps = 17/685 (2%)

Query: 34 PSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVFKFCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPAA TV+F+CP++G P
 Sbjct: 129 PSSGDEDGED-----EAEDTGVDTGAPYWRPERMDKKLLAVPAANTVFRCPAAGNP 182

Query: 94 NPTLRWLNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQWSSLVMSVVPSDRGNYTCVVENKFGSIRQTYT 242

Query: 154 LDVVERSPHRPIQAGLPANKTVALGSNVEPMCKVYSDPQPHIQOWLKHIEVNGSKIGPDN 213
 LDV+ERSPHRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQOWLKH+EVNGSK+GPD
 Sbjct: 243 LDVLERSPHRPILQAGLPANQTAVLGSVDFHCKVYSDAQPHQOWLKHIEVNGSKVGPDG 302

Query: 214 LPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYICEANQSAWLTTRPVAK 271
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +
 Sbjct: 303 TPYVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHSAWLVVL-PAEE 361

Query: 272 ALEERPAVMTSPLYLEIICTGAFLICMLGSVIIYKMKSGTKKSDFHQSMAVHKLAKS 331
 L E A +Y I+ Y G FL ++ +V + +++S KK VHKK++
 Sbjct: 362 ELVE--ADEAGSVYAGILSYGVGFILFLVVAATLCRLRSPPKG--LGSPTVHKISR- 416

Query: 332 IPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 391
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L
 Sbjct: 417 FPLKRQV--SLESNASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSARLTL 474

Query: 392 GKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKMLKSDATEKDLSDLISEMEMMMKIGK 451
 GKPLGEGCFGQVW+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMMKIGK
 Sbjct: 475 GKPLGEGCFGQVVMAEAIGIDKDRAAKPVTAVKMLKDDATDKDLSDLVSEMEMMMKIGK 534

Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQQLSSKDL 511
 HKNIINLL ACTQ GPLYV+VEYA-KGNLRE+L+ARRPPGL+Y ++ PEEQ+ KDL
 Sbjct: 535 HKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEQLTFKDL 594

Query: 512 VSCAYQVARGMEYLASKKCIIHDLAARNVLVTEDNVMKIADFGLARDIH+DYYKKTTNG 571
 VSCAYQVARGMEYLAS+KCIIHDLAARNVLVTEDNVMKIADFGLARD+H++DYYKKTTNG
 Sbjct: 595 VSCAYQVARGMEYLASQKCIHDLAARNVLVTEDNVMKIADFGLARDVHNLDYYKKTTNG 654

Query: 572 RLPVKWMAPEALFDRIYTHQSDWVSGVLLWEITLGGSPYPGVVEELFKLLKEGHHRMD 631
 RLPVKWMAPEALFDR+YTHQSDWVSGVLLWEITLGGSPYPG+PVEELFKLLKEGHHRMD
 Sbjct: 655 RLPVKWMAPEALFDRVYTHQSDWVSGVLLWEITLGGSPYPGIPVVEELFKLLKEGHHRMD 714

Query: 632 KPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSF 691
 KP+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
 Sbjct: 715 KPANCTHDLYMIMRECWAHAPSQRPTFKQLVEDLDRVLTSTDEYLDLSAPFEQYSPGG 774

Query: 692 PDTRSSTCSSGEDSVFSHEPLPEEP 716
 DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 775 QDTPSSS-SSGDDSVFAHDLLPPAP 798

tr Q8NI15 Fibroblast growth factor receptor 3 (Fragment) [FGFR3] [Homo sapiens (Human)] align

Score = 931 bits (2406), Expect = 0.0
 Identities = 462/685 (67%), Positives = 552/685 (80%), Gaps = 17/685 (2%)

Query: 34 PSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVFKFCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPAA TV+F+CP++G P
 Sbjct: 92 PSSGDEDGED-----EAEDTGVDTGAPYWRPERMDKKLLAVPAANTVFRCPAAGNP 145

Query: 94 NPTLRWLNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 146 TPSISWLKNGREFRGEHRIGGIKLRHQWSSLVMSVVPSDRGNYTCVVENKFGSIRQTYT 205

Query: 154 LDVVERSPHRPIQAGLPANKTVALGSNVEPMCKVYSDPQPHIQOWLKHIEVNGSKIGPDN 213
 LDV+ERSPHRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQOWLKH+EVNGSK+GPD
 Sbjct: 206 LDVLERSPHRPILQAGLPANQTAVLGSVDFHCKVYSDAQPHQOWLKHIEVNGSKVGPDG 265

Query: 214 LPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYICEANQSAWLTTRPVAK 271
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +
 Sbjct: 266 TPYVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHSAWLVVL-PAEE 324

Query: 272 ALEERPAVMTSPLYLEIICTGAFLICMLGSVIIYKMKSGTKKSDFHQSMAVHKLAKS 331
 L E A +Y I+ Y G FL ++ +V + +++S KK VHKK++
 Sbjct: 325 ELVE--ADEAGSVYAGILSYGVGFILFLVVAATLCRLRSPPKG--LGSPTVHKISR- 379

Query: 332 IPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 391
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L
 Sbjct: 380 FPLKRQV--SLESNASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSARLTL 437

Query: 392 GKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKMLKSDATEKDLSDLISEMEMMMKIGK 451
 GKPLGEGCFGQVW+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMMKIGK

Sbjct: 438 GKPLGEGCFGQVMAEAIGIDKDRAAKPVTVAVKMLKDDATDKLSDLVSEMEMMKMICK 497
 Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDL 511
 HKNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL
 Sbjct: 498 HKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQLTFKDL 557
 Query: 512 VSCAYQVARGMEYLASKKCIRHDLAARNVLVTEDNVMKIADFGLARDIHHDYKKTTNG 571
 VSCAYQVARGMEYLAS+KC1HDLAARNVLVTEDNVMKIADFGLARD+H++DYKKTTNG
 Sbjct: 558 VSCAYQVARGMEYLASQKCIIRHDLAARNVLVTEDNVMKIADFGLARDVHNLDYKKTTNG 617
 Query: 572 RLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMD 631
 RLPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKEGHRMD
 Sbjct: 618 RLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMD 677
 Query: 632 KPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRLIVALTSNQEYLDLSIPLDQYSPSF 691
 KP+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
 Sbjct: 678 K PANCTHDLYMIMRECWAAPSQRPTFKQLVEDLDRVLTSTDEYLDLSAPFEQYSPGG 737
 Query: 692 PDTRSSTCSSGEDSVFSHEPLPEEP 716
 DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 738 DTPSSS-SSGDDSVFAHDLLPPAP 761

tr Q8NI16 Fibroblast growth factor receptor 3 (Fragment) [FGFR3] [Homo sapiens (Human)] align

Score = 929 bits (2402), Expect = 0.0
 Identities = 459/684 (67%), Positives = 551/684 (80%), Gaps = 13/684 (1%)
 Query: 34 PSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKEMKKLHAVPAAKTVKFKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P
 Sbjct: 92 PSSGDDEDGED-----EAEDTGVDTGAPYWRPERMDKKLLAVPAANTVRFRCPAAGNP 145
 Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS+M+SVVPSD+GNYTC+VEN+CSI TY
 Sbjct: 146 TPSISWLKNGREFRCEHRRIGGIKLRHQQWSLVMESVVPSDRGNYTCVVENKFGSIRQTYT 205
 Query: 154 LDVVERSPHRPILOQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
 LDV+ERSPHRPILOQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
 Sbjct: 206 LDVLERSPHRPILOQAGLPANQTAVLGSDFEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDG 265
 Query: 214 LPVVQILKHSGINSSDAEV-LTLFNVTEAQSGEYVCKVSNYIIGEANQSAWLTVTRPVAKA 272
 PYV +LK S +A+V L N V+E GEY+C+ +N+IG A ++ WL+V P A
 Sbjct: 266 TPYVTVLKSWISESVEADVRLRLANVSERDGEYLCRATNFIGVAEKAFWLSVHGPRAAE 325
 Query: 273 LBERPAVMTSPLYLEIIIYCTGAFLISCMLGSVIYKMKSGTKSDFHSQMAVHKLAJKSI 332
 E A +Y I+ Y G FL ++ +V + ++S KK VHK+++
 Sbjct: 326 EELVEADEAGSVYAGILSYGVGFFLFLVVAATVLCRLRSPPKKG--LGSPTVHKISR-F 382
 Query: 333 PLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLG 392
 PL+RQV S +S+ASM+S LRV +RLSS P LA VSE ELP DP+WEL R RL LG
 Sbjct: 383 PLRKVR--SLESNAMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTLC 440
 Query: 393 KPLGEFCFGQVVAEAIQLDKDPNRTVKAVKMLKSDATEKDLSLDLISEMEMMMKMICGH 452
 KPLGEFCFGQVV+AFAIG+DKD+ + VAVKMLK DAT+KDLSLDLISEMEMMMKMICGH
 Sbjct: 441 KPLGEFCFGQVVAEAIQIDKDRAAKPVTVAVKMLKDDATDKLSDLVSEMEMMMKMICGH 500
 Query: 453 KNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLV 512
 KNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLV
 Sbjct: 501 KNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQLTFKDLV 560
 Query: 513 SCAYQVARGMEYLASKKCIRHDLAARNVLVTEDNVMKIADFGLARDIHHDYKKTTNGR 572
 SCAYQVARGMEYLAS+KC1HDLAARNVLVTEDNVMKIADFGLARD+H++DYKKTTNGR
 Sbjct: 561 SCAYQVARGMEYLASQKCIIRHDLAARNVLVTEDNVMKIADFGLARDVHNLDYKKTTNGR 620
 Query: 573 LPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMDK 632
 LPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKEGHRMDK
 Sbjct: 621 LPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMDK 680
 Query: 633 PSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRLIVALTSNQEYLDLSIPLDQYSPSF 692
 P+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
 Sbjct: 681 PANCTHDLYMIMRECWAAPSQRPTFKQLVEDLDRVLTSTDEYLDLSAPFEQYSPGGQ 740
 Query: 693 DTRSSTCSSGEDSVFSHEPLPEEP 716
 DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 741 DTPSSS-SSGDDSVFAHDLLPPAP 763

sp_vs P22607-2 Isoform 2 of P22607 - Homo sapiens (Human) [FGFR3] [Homo sapiens 808 AA align
 FGFR3_HUMAN (Human)]

Score = 929 bits (2402), Expect = 0.0
 Identities = 459/684 (67%), Positives = 551/684 (80%), Gaps = 13/684 (1%)

Query: 34 PSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPAAV TV+F+CP++G P
 Sbjct: 129 PSSGDEDGED-----EAEDTGVDTGAPWTRPERMDKKLLAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS+M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQWSLVMESVPSDRGNYTCVVENKFGSIRQTYT 242

Query: 154 LDVVERSPHRPILOAGLPANKTVALGSNVEPMCKVYSDPQPHIQOWLKHIEVNGSKIGPDN 213
 LDV+ERSRHPILQAGLPAN+T LGS+VEF CKVYSD QPHIQOWLKHIEVNGSK+GPD
 Sbjct: 243 LDVLERSPHRPILOAGLPANQTAVLGSDVEFHCKVYSDAQPHIQOWLKHIEVNGSKVGPDG 302

Query: 214 LPYVQILKHSGINSSDAEV-LTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTTRPVAKA 272
 PYV +LK S +A+V L L NV+E CEY+C+ +N+IG A ++ WL+V P A
 Sbjct: 303 TPYVTVLKSWISESVEADVRLRLANVSERDGGEYLCRATNFIGVAEKAFWLSPVHGPRAAE 362

Query: 273 LEERPAVMTSPLYLEIIIICTGAFLISCMLGSVIYKMKSGTKKSDFHQSMAVHKLAKSI 332
 E A +Y I+ Y G FL ++ +V + +++S KK VHK+++
 Sbjct: 363 EELVEADEAGSVYAGILSYGVGFFILFILVVAATVTLCLRSPPKKG--LGSPTVHKISR-F 419

Query: 333 PLRRQTVTSADSSASMNSGVLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRVLG 392
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL LG
 Sbjct: 420 PLKRQV--SLESNASMSNTPLVRIARLSSGCGPTLANVSELELPADPKWELSRARLTG 477

Query: 393 KPLGEFGCFQVVLAEAIGLDKDPNRTVKAVKMLKSDATEKDLSLDLISEMEMMMKIGKH 452
 KPLGEFGCFQVVAEAIIG+DKD+ + VAVKMLK DAT+KDLSLD+SEMEMMMKIGKH
 Sbjct: 478 KPLGEFGCFQVVMMEAIGIDKDRRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMMKIGKH 537

Query: 453 KNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLV 512
 KNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLV
 Sbjct: 538 KNIINLLGACTQQGGLPLYVLVEYAAKGNLREFLARRPPGLDYSFDTCKPPEQLTFKDLV 597

Query: 513 SCAYQVARGMEYLAASKKCIHRLAARNVLVTEDNVVMKIADFGLARDIHHDYYKTTNGR 572
 SCAYQVARGMEYLAS+KCIHRLAARNVLVTEDNVVMKIADFGLARD+H+DYYKTTNGR
 Sbjct: 598 SCAYQVARGMEYLAQKCIHRLAARNVLVTEDNVVMKIADFGLARDVHNLDYYKTTNGR 657

Query: 573 LPVKWMAPEALFDRIYTHQSDWVWSFGVLLWEITLGGSPYPGVVPVEELFKLLKEGHRMDK 632
 LPVKWMAPEALFDR+YTHQSDWVWSFGVLLWEITLGGSPYPG+PVEELFKLLKEGHRMDK
 Sbjct: 658 LPVKWMAPEALFDRVYTHQSDWVWSFGVLLWEITLGGSPYPGIPVEELFKLLKEGHRMDK 717

Query: 633 PSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSF 692
 P+NCT++LYM+MR+CWAH PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
 Sbjct: 718 PANCTHDLYMIMRECWHAAPSQRPTFKQLVEDLDRVLTSTDEYLDLSAPFEQYSPGGQ 777

Query: 693 DTRSSTCSSLGEDSVFSHEPLPEEP 716
 DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 778 DTPSSS-SSGDDSVFAHDLPPPAP 800

sp_vs_P11362-9 Isoform 5 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 660 AA align

Score = 926 bits (2393), Expect = 0.0
 Identities = 466/503 (92%), Positives = 477/503 (94%), Gaps = 10/503 (1%)

Query: 31 DALPSSSEDDDDDDSSSEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSSEDDDDDDSSSEEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 120 DALPSSSEDDDDDDSSSEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGS 148
 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGS
 Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGS 239

Query: 149 NHTYQLDVVERSOPHRPILOAGLPANKTVALGSNVEPMCKVYSDPQPHIQOWLKHIEVNGSK 208
 NHTYQLDVVERSOPHRPILOAGLPANKTVALGSNVEPMCKVYSDPQPHIQOWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVVERSOPHRPILOAGLPANKTVALGSNVEPMCKVYSDPQPHIQOWLKHIEVNGSK 299

Query: 209 IGPDNLPVQILKHSGINSSDAE--VLTIFNVTTEAQSGEYVCKVSNYIGEANQSAWLT 266
 IGPDNLPVQILK+G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDNLPVQILKTAGVNNTDKEMEVHLRNVSFEDAGEYTCLAGNSIGLSSHSAWLTVL 359

Query: 267 RPVAKALEERPAVMTSPLYLEIIIICTGAFLISCMLGSVIYKMKSGTKKSDFHQSMAVH 326
 +ALEERPAVMTSPLYLEIIIICTGAFLISCM+GSVI+YKMKSGTKKSDFHQSMAVH
 Sbjct: 360 -----EALEERPAVMTSPLYLEIIIICTGAFLISCMVGSVIVYKMKSGTKKSDFHQSMAVH 415

Query: 327 KLAKSIPLRQTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAKSIPLRQV SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAKSIPLRQV---SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 473

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKMLKSDATEKDLSLDLISEMEMM 446
 DRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKMLKSDATEKDLSLDLISEMEMM

Spjct: 474 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 533
 Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPSEEQL 506
 KMICKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPSEEQL
 Spjct: 534 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPSEEQL 593
 Query: 507 SSKDLVSCAYQVARGMEYLASKK 529
 SSKDLVSCAYQVARGMEYLASKK
 Spjct: 594 SSKDLVSCAYQVARGMEYLASKK 616

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSSSEDDDDDSSEEKETDNTKPNSPV 60
 MW WKCLLFWAVLVTATLCTARP+PTLPEQ
 Spjct: 1 MWSWKCLLFWAVLVTATLCTARPSPALPEQ----- 30

Query: 61 APYWTSSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFPDPHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL+G + +R R
 Spjct: 31 AQPWGAPVEVESPL--VHPGDLQLRCRLRDDVQ-SINWLRDGVLQABSNR----TRIT 82

Query: 121 TWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSP----- 161
 + + VP+D G Y C + GS + ++V + P
 Spjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVDALPSSSEDDDDDSSEEKETD 142

Query: 162 ----HRPILQAGLANK-----TVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 P+ K V V+F C P P ++WLK NG +
 Spjct: 143 NTKPNRMPVAPYWTSSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLK---NGKEFK 198

Query: 211 PDNLPLYVQILKHSGINSSDAEVTLTFNUTEAQSGEYVCKVSNYIGEANQSAWLTVT--- 266
 PD+ +++ + + + +V + G Y C V N G N + L V
 Spjct: 199 PDHRIGGYKVRYATWS----IIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSP 252

Query: 267 -RPVAKA 272
 RP+ +A
 Spjct: 253 HRPILQA 259

Spjct: P11362-12 Isoform 11 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 502 AA align
 FGFR1_HUMAN (Human)]

Score = 857 bits (2214), Expect = 0.0
 Identities = 429/462 (92%), Positives = 440/462 (95%), Gaps = 6/462 (1%)

Query: 70 MEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFPDPHRIGGYKVRYATWSIIMDSV 129
 MEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFPDPHRIGGYKVRYATWSIIMDSV
 Spjct: 1 MEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFPDPHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 189
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY
 Spjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKHSGINSSDAE--VLTLFNVTTEAQSGEYV 247
 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILK +G+N+D E VL L NV+ +GEY
 Spjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLPLYVQILKTAGVNNTDKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIYCTGAFLISCMLGSVII 307
 C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIYCTGAFLISCM+GSVI+
 Spjct: 181 CLAGNSIGLSSHSAWLTVL---EALEERPAVMTSPLYLEIIIYCTGAFLISCMVGSVIV 236

Query: 308 YKMKSGTJKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPM 367
 YKMKSGTJKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPM
 Spjct: 237 YKMKSGTJKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPM 296

Query: 368 LAGVSEYELPEDPRWELPRDRVLVGLKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
 LAGVSEYELPEDPRWELPRDRVLVGLKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML
 Spjct: 297 LAGVSEYELPEDPRWELPRDRVLVGLKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 356

Query: 428 KSDATEKDLSDLISEMEMMMKMGHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
 KSDATEKDLSDLISEMEMMMKMGHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR
 Spjct: 357 KSDATEKDLSDLISEMEMMMKMGHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 416

Query: 488 RPPGLEYCYNPSHNPSEEQLSSKDLVSCAYQVARGMEYLASKK 529
 RPPGLEYCYNPSHNPSEEQLSSKDLVSCAYQVARGMEYLASKK
 Spjct: 417 RPPGLEYCYNPSHNPSEEQLSSKDLVSCAYQVARGMEYLASKK 458

Spjct: P11362-13 Isoform 13 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 500 AA align
 FGFR1_HUMAN (Human)]

Score = 848 bits (2192), Expect = 0.0
 Identities = 427/462 (92%), Positives = 438/462 (94%), Gaps = 8/462 (1%)

Query: 70 MEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129
 MEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV
 Sbjct: 1 MEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 189
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVY 120

Query: 190 SDPOPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAE--VLTLFNVTTEAQSGEYV 247
 SDPOPHIQWLKHIEVNGSKIGPDNLPYVQILK +G+N+D E VL L NV+ +GEY
 Sbjct: 121 SDPOPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNNTDKEMEVLHRLNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMGSVII 307
 C N IG ++ SAWLTV +ALEERPAVMTSPLYLEIIIIYCTGAFLISCM+GSVII+
 Sbjct: 181 CLAGNSIGLSHHSAWLTVL---EALEERPAVMTSPLYLEIIIIYCTGAFLISCMGSVIV 236

Query: 308 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSPRLSSSGTPM 367
 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVRPSPRLSSSGTPM
 Sbjct: 237 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVRPSPRLSSSGTPM 294

Query: 368 LAGVSEYELPEDPDRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKML 427
 LAGVSEYELPEDPDRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKML
 Sbjct: 295 LAGVSEYELPEDPDRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKML 354

Query: 428 KSDATEKDLSDLISEMEMMMKIGKHNIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
 KSDATEKDLSDLISEMEMMMKIGKHNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR
 Sbjct: 355 KSDATEKDLSDLISEMEMMMKIGKHNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 414

Query: 488 RPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKK 529
 RPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKK
 Sbjct: 415 RPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKK 456

sp P22455 Fibroblast growth factor receptor 4 precursor (EC 2.7.10.1) 802 AA
 FGFR4_HUMAN (FGFR-4) (CD334 antigen) [FGFR4] [Homo sapiens (Human)] align

Score = 839 bits (2168), Expect = 0.0
 Identities = 432/707 (61%), Positives = 527/707 (74%), Gaps = 29/707 (4%)

Query: 18 LCTARPAP-----TLPEQDALPSSSEDDDDSSSEEKETDNTKPNPVAPYWTSPKME 71
 LC AR + TL D+L SS +DD+D S + ++ P APYWT P++ME
 Sbjct: 100 LCLARGSMIVLQNLTITGDSLTS--NDDEDPKSHRDPNSRHSYPQQ-AFYWTHPQRME 156

Query: 72 KKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 131
 KKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG ++R+ WS++M+SVVP
 Sbjct: 157 KKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDQAFHGENRIGGIRLHQHWSLVMESVVP 216

Query: 132 SDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSD 191
 SD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD
 Sbjct: 217 SDRGTYTCLVENAVGSIRYNYLLDVLERSPHRPILQAGLPANTTAVVGSDELLCKVYSD 276

Query: 192 PQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAEVLTFNVTTEAQSGEYVCKVS 251
 QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C
 Sbjct: 277 AQPHIQWLKHIVINGSSFGADGFPYVQVQLKTADINSVEVLYRNVSaedageytclag 336

Query: 252 NYIGEANQSAWLTVTRPVAKALEERP---AVMTSPLYLEIIIIYCTGAFLISCMGSVIIY 308
 N IG + QSAWLTVA EE P A Y +II+Y +G+ ++ +L +Y
 Sbjct: 337 NSIGLSYQSAWLTVLP-----EEDPTWAAPEARYTDIILYASGSLALAVLLLLLAGLY 390

Query: 309 KMKGSTKKSDFHSQ--MAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSPRLSSSGTP 366
 + G H + V KL++ PL RQ ++ + SS +S LVR RLSSSG
 Sbjct: 391 R---GQALHGRHPRPPATVQKLSR-FPLARQPSLESGGSSGKSSSS--LVRGVRLSSSGPA 444

Query: 367 MLAGVSEYELPEDPDRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDPNRTKVAVKML 426
 +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVVLAEAIGD+P++ + VAVKM
 Sbjct: 445 LLAGVLSLDLPLWEPFPRDRLVLGKPLGEGCFGQVRAEAFGMDPARPDQASTVAVKML 504

Query: 427 LKSDATEKDLSDLISEMEMMMKIGKHNIINLLEACTQDGPLYVIVEYASKGNLREYLQA 486
 LK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLVIVE A+KGNLRE+L+A
 Sbjct: 505 LKDNASDKDLADLVSEMEVMKLIIGRHKNIINLLGVCTQEGPLVIVECAAKGNLREFLRA 564

Query: 487 RRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDN 546
 RRPPG + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDN
 Sbjct: 565 RRPPGPDLSPDGRSSEGPLSPFVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDN 624

Query: 547 VMKIADFGLARDIHIDYYKKTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEIFT 606
 VMKIADFGLAR +HHIDYYKKT+NGRLPVKWMMAPEALFDRIYTHQSDVWSFG+LLWEIFT
 Sbjct: 625 VMKIADFGLARGVHHIDYYKKTNSNGLPVKWMMAPEALFDRIYTHQSDVWSFGILLWEIFT 684

Query: 607 LGGSPYPGPVVEELFKLLKEGHMRMDKPSNCTNELYMMMRDCWHAPSQRPTFKQLVEVLD 666
 LGGSPYPGP+VEELF LL+EGRHMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD

Subject: 685 LGGSPYPGIPVEELFSLLREGHMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALD 744
 Query: 667 RIVALTSNQEYLDLSIPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLP 713
 +++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP
 Subject: 745 KVL-LAVSEEEYLRLTGFYSPSGGDA-SSTCSS-SDSVFSHDPLP 788

tr Q8TDAO Fibroblast growth factor receptor 4 (Fibroblast growth factor receptor 4, isoform CRA_b) [FGFR4] [Homo sapiens (Human)] 802 AA align

Score = 839 bits (2167), Expect = 0.0
 Identities = 432/707 (61%), Positives = 527/707 (74%), Gaps = 29/707 (4%)

Query: 18 LCTARPAP-----TLPEQDALPSSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKME 71
 LC AR + TL D+L SS +DD+D S + ++ P APYWT P++ME
 Subject: 100 LCLARGSMIVLQNLTLITGDSLTS--NDDEDPKSHRDLSNRHSYPQQ-APYWTHPQRME 156

Query: 72 KKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 131
 KKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG ++R+ WS++M+SVVP
 Subject: 157 KKLHAVPAGNTVKFRCPAAGNPPTIRWLKDQAFHGENRIGGIRLHQHWSLVMSVVP 216

Query: 132 SDKNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSD 191
 SD+G YTC-VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD
 Subject: 217 SDRGTYTCLVENAVGSIRINYLLDVLERSPHRPILQAGLPANTTAVVGSDVELLCKVYSD 276

Query: 192 PQPHIQWLKHIEVNGSKIGPDNLQVQIQLKHSGINSSDAEVLTLFNVTEAQSGEYVCKVS 251
 QPHIQWLKH +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C
 Subject: 277 AQPHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAG 336

Query: 252 NYIGEANQSAWLTVTRPVAKALEERP---AVMTSPLYLEIIIIYCTGAFLISCMGLSVIIY 308
 N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L +Y
 Subject: 337 NSIGLSYQSAWLTVLP-----EEDPTWTAAAPEARYTDIILYASGSLALAVLLLALAGLY 390

Query: 309 KMKGSTKKSDHSQ--MAVHKLAKSIPLRRQTVTSADSSAMNSGVLLVRPSRLSSSGTP 366
 + G H + V KL++ PL RQ ++ + SS +S LVR RLSSSG
 Subject: 391 R---CQALHGRHPRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRLSSSGPA 444

Query: 367 MLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAAEIALDKDKPNRVTKAVKM 426
 +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKM
 Subject: 445 LLAGLVSDLPLDPLWEFPRDRLVLGKPLGEGCFGQVVRRAEAFGMDPARPDQASTVAVKM 504

Query: 427 LKSDATEKDLSLDISEMEMMMKIMGKHKNIINILLEACTQDGPLYVIVEYASKGNLREYLQA 486
 LK +A++KDL+DL+SME+MK+IG+HKNI+INLL CTG+GPLYVIVE A+KGNLRE+L+A
 Subject: 505 LKDNASDKLADLVSEMEVMKLIGHHKNIINLLGVCCTQECGVTCIVECAKGNLREFLRA 564

Query: 487 RRRPGLEYCYNFSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDN 546
 RRRPG + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDN
 Subject: 565 RRRPGPDLSLSPDGRSSEGPLSFPVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDN 624

Query: 547 VMKIADPGLARDIHIDYYKTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVILLWEIFT 606
 VMKIADPGLAR +HHIDYYKKT+NGRLPVKWMMAPEALFDR+YTHQSDVWSFG+LLWEIFT
 Subject: 625 VMKIADPGLARGVHHIDYYKKTNSNGLRPLVKWMMAPEALFDRVYTHQSDVWSFGILLWEIFT 684

Query: 607 LGGSPYPGVPVEELFKLLKEGHMDKPSNCNTNELYMMMRDCWHAVPSQRPTFKQLVEVLD 666
 LGGSPYPG+PVEELF LL+EGRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD
 Subject: 685 LGGSPYPGIPVEELFSLLREGHMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALD 744

Query: 667 RIVALTSNQEYLDLSIPLDQYSPSFPDTRSSTCSSGEDSVFSHEPLP 713
 +++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP
 Subject: 745 KVL-LAVSEEEYLRLTGFYSPSGGDA-SSTCSS-SDSVFSHDPLP 788

tr Q71TWS Fibroblast growth factor receptor 4, soluble-form splice variant 762 AA align
 Q71TWS_HUMAN [FGFR4] [Homo sapiens (Human)]

Score = 805 bits (2078), Expect = 0.0
 Identities = 414/700 (59%), Positives = 501/700 (71%), Gaps = 55/700 (7%)

Query: 18 LCTARPAPTLPEQDAL---PSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPKMEKK 73
 LC AR + + + L S+ +DD+D S + ++ P APYWT P++MEKK
 Subject: 100 LCLARGSMIVLQNLTLITGDSLTSNNDEDPKSHRDLSNRHSYPQQ-APYWTHPQRMEKK 158

Query: 74 LHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 133
 LHAVPA TVKF+CP++G P PT+RWLK+G+ F +RIGG ++R+ WS++M+SVVPSD
 Subject: 159 LHAVPAGNTVKFRCPAAGNPPTIRWLKDQAFHGGNRIGGIRLHQHWSLVMESVVP 218

Query: 134 KGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQ 193
 +G YTC-VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD Q
 Subject: 219 RGTYTCLVENAVGSIRINYLLDVLERSPHRPILQAGLPANTTAVVGSDVELLCKVYSDAQ 278

Query: 194 PHIQLWKHIEVNGSKIGPDNLFPYQILKHSGINSSDAEVLTLPNVTEAQSGEYVCKVSNY 253
 PHIQLWKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C N
 Sbjct: 279 PHIQLWKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVS AEDAGEYTCLAGNS 338

Query: 254 IGEANOSAWLTVTRPVAKALEERPAVMTSPLYLEIIYCTGAFLISCMGLGSVIIYKMKSG 313
 IG + QSAWLTV P P + C + + ++SG
 Sbjct: 339 IGLSYQSAWLTVL-----PGTGRIP-----HLTCDSLTPAGRKSPTLQFSLESG 383

Query: 314 TKSDFHQSOMAVHKLAKSIPPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSE 373
 + S SS+S LVR RLSSSG +LAG+
 Sbjct: 384 S-----SGKSSSS-----LVRGVRLSSSGPALLAGLVS 411

Query: 374 YELPEDPRWELPDRDLVLGKPLGEGCFQVVI AEAIGLDKDKPNRVTKAVKMLKSDATE 433
 +LP DP WE PRDRLVLGKPLGEGCFQVVI AEA G+ +P++ + VAVKMLK +A++
 Sbjct: 412 LDLPLDPLWEFPRDRLVLGKPLGEGCFQVVRRAEAFGMDPARPDQASTAVAKMLKDNASD 471

Query: 434 KDLSDLISEMEMMMKIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLE 493
 KDL+DL+SEME+MK+IG+HKNIINLL CTQ+CPLYVIVE A+KGNLRE+L+ARRPPG +
 Sbjct: 472 KDLADLVSEMEVMKLIGRHKNIINLLGVCQEGLPLYVIVECAAKGNLREFLRARPPGP 531

Query: 494 YCYNPSHNPPEEQLSSKDLVSCAYQVARGMEYIASKKCIHRLDAARNVLVTEDNVMKIADF 553
 + + E LS LVSCAYQVARGM+YL S+KCIHRLDAARNVLVTEDNVMKIADF
 Sbjct: 532 LSPDGPRSSEGPLSFVVLVSCAYQVARGMOYLESRKCIHRLDAARNVLVTEDNVMKIADF 591

Query: 554 GLARDIHHIDYYKKTTNGRLPKWMAPEALFDRYITHQSDVWSFGVLLWEIFTLGGSPYP 613
 GLAR +HHIDYYKKT+NGRLPKWMAPEALFDR+YTHQSDVWSFG+LLWEIFTLGGSPYP
 Sbjct: 592 GLARGVHHIDYYKKTSNGRLPKWMAPEALFDRVYTHQSDVWSFGILLWEIFTLGGSPYP 651

Query: 614 GVPVEEFLKLLKEHRMDKPSNCTNELYMMMRDCWAVPSQRPTFKQLVEVLDRIVALTS 673
 G+PVEEFL LL+EGHRMD+P +C ELY +MR+CWAH PSQRPTFKQLVE LD++ L
 Sbjct: 652 GIVPEEFLSLLREGRHMDRPPHCPELYGLMRECWHAPSQRPTFKQLVEALDKVL-LAV 710

Query: 674 NQEYLDLSIPLDQYSPSFPDTRSSTCGGEDSVFSHEPLP 713
 ++EYLDL + YSPS D SSTCSS DSVFSH+PLP
 Sbjct: 711 SEEYLDLRLTFGPYSPSGGDA-SSTCSS-SDSVFSHDPLP 748

tr Q8IXC7 Isoform of FGFR2 [FGFR2 AT-I] [Homo sapiens (Human)] 709 AA
 Q8IXC7_HUMAN align

Score = 770 bits (1989), Expect = 0.0
 Identities = 420/753 (55%), Positives = 502/753 (66%), Gaps = 83/753 (11%)

Query: 1 MWGKCLLFWAVLVTATLCTARPAPTLPEQDALPSSEDDDDDSSEEKETDNTKPNPV 60
 M W + V+ ATL ARP+ +L E L E P
 Sbjct: 1 MVSWRFRFICLVVVTMATLSLARPSFSLVEDTLEPEE-----PP 39

Query: 61 APYWTSSPEKMEKKLHAVPAAKTVFKFCPSSGTPNPTLRLWLNKGKEFKPDHR--IGGYKV 117
 Y S + +++ + + + +C + W K+G P++R IG Y
 Sbjct: 40 TKYQIS----QPEVYVAAPGESLEVRCLLKDA--VISWTKDGVHLPNNRTVLIQEY-- 91

Query: 118 RYATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVE----- 158
 + + P D G Y C S + + +V +
 Sbjct: 92 -----LQIKGATPRDGLYACTASRTVDSETWYFMVNVTDAISSGDEDDTDGAEDFVS 145

Query: 159 -----RSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
 R+P+ + V + V+F C +P P + +WLX NG + +
 Sbjct: 146 ENSNNKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLK---NGKEFKQE 201

Query: 213 NLPYVQILKHSGINSSDAE-VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTTRPVAK 271
 + + G + L + +V + G Y C V N G N + L V P
 Sbjct: 202 H-----RIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSINHTYHLDVVAP--- 251

Query: 272 ALEERPAVMTSPLYLEIIYCTGAFLISCMGLGSVIIYKMKSGTKKSDFHQSOMAVHKLAKS 331
 + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 252 --GREKEITASPDYLEIAIYICGVFLIACMVVTILCRMKNNTKKPDFSSQPAVHKLTKR 309

Query: 332 IPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDRL 389
 IPLRRQVTSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L
 Sbjct: 310 IPLRRQVTSAESSSSMSNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPRDKL 369

Query: 390 VLGPLGEGCFQVVLAEAIGLDKDKPNRVTKAVKMLKSDATEKDLSDLISEMEMMMKMI 449
 LGKPLGEGCFQVVAEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMMKMI
 Sbjct: 370 TLGPLGEGCFQVVMMAEVGIDDKDPKEAVKMLKDDATEKDLSDLVSEMEMMMKMI 429

Query: 450 GKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPPEEQLSSK 509
 GKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++ K
 Sbjct: 430 GKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTFK 489

Query: 510 DLVSCAYQVARGMEYLASKKCIHRLDAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTT 569
 DLVSC YQ+ARGMEYLAS+KCIHRLDAARNVLVTE+NVMKIADFGLARDI++IDYYKKTT
 Sbjct: 490 DLVSCTYQLARGMEYLASQKCICHRLDAARNVLVTEENNVMKIADFGLARDINNIDYYKKTT 549

Query: 570 NGRLPKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHR 629
 NGRLPKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHR

Sbjct: 550 NGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIPTLGGSPYPGIPVEELFKLLKEGHR 609
 Query: 630 MDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDSIPLDQYSP 689
 MDKP+NCNTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYSP
 Sbjct: 610 MDK PANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEQYSP 669
 Query: 690 SFDPDTRSSSTCSSLGEDSVFSHEPLPEEPCLPRHP 722
 S+PDTRSS CSSG+DSVFS +P+P EPCLP+P
 Sbjct: 670 SYPDTRSS-CSSGDDSVFSPDPMYEPCLPQYP 701

tr Q96KE5 Fibroblast growth factor receptor 4 variant [Homo sapiens (Human)] 592 AA
 Q96KE5_HUMAN align

Score = 735 bits (1898), Expect = 0.0
 Identities = 377/593 (63%), Positives = 452/593 (76%), Gaps = 20/593 (3%)
 Query: 126 MDSVVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFM 185
 M+SVVPSD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +
 Sbjct: 1 MESVVPSDRGTYTCLVENAVGSIRYNLDDVLERSPHRPILQAGLPANTTAVVGSDVELL 60
 Query: 186 CKVYSDPQPHIQWLKHIEVNGSKIGPDNLPVYQILKHSGINSSDAEVLTLFNVTEAQSGE 245
 CKVYSD QPHIQWLKH +NCS G D PVVO+LK + INSS+ EVL I NV+ +GE
 Sbjct: 61 CKVYSDAQPQHQWLKHIVINGSSFGADGFPPVYQVLKTADINSSEEVLYLRNVAEDAGE 120
 Query: 246 YVCKVSNVYIGEANQSAWLTVTPVAKALEERP---AVMTSPLYLEIIIYCTGAFLISML 302
 Y C N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L
 Sbjct: 121 YTCLAGNSIGLSYQSAWLTVP-----EEDPTWTAAAPEARYTDIILYASGSLALAVL 174
 Query: 303 GSVIYKMKSGTKKSDFHSQ--MAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRL 360
 ++ ++ G H + V KL++ PL RQ ++ +S +S LVR RL
 Sbjct: 175 ---LLARLYRGQALHGRHPRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRL 228
 Query: 361 SSSGTPMILAGVSEYELPDEPFWELPRDRRLVLCPLGEGCCFGQVVAEIGLDKDKNRVT 420
 SSSG +LAG+ +LP DP WE PRDRRLVLCPLGEGCCFGQVVA AEA G+D +P++ +
 Sbjct: 229 SSSGPALLAGLVSLDPLPDLWEPFRDRRLVLCPLGEGCCFGQVRAEAFGMDPARDQAS 288
 Query: 421 KVAVKMLKSDATEKDLSSDLISEMEMMKMIGKHKNIINNLEACTQDGPLYVIVEYASKGNL 480
 VA VAKMLK +A+A+KDL+DL+SEM+MK+IG+HKNIINNL CTQ+GPLYVIVE A+KGNL
 Sbjct: 289 TVAVKMLKDNASDKDLADLVSEMEVMKLIGRHKNIINLLGVCTQEGPLYVIVECAAKGNL 348
 Query: 481 REYLQARRPPGLEYCYNPSHNPEEQQLSSKKDLVSCAYQVARGMEMYLASKKCIHRLAARNV 540
 RE+L+ARRPPG + + + E LS LVSCAYQVARGM+YL S+KCIHRLAARNV
 Sbjct: 349 REFLRARRPPGPDLSPDGRSSEGPLSFVLSVSCAYQVARGMQYLESRKCIHRLAARNV 408
 Query: 541 LVTEDNVMKIAFDGLARDIHIDYYKKTTNGRLPVKWMMAPEALFDRYTHQSDVWSFGVL 600
 LVTEDNVMKIAFDGLAR +HHIDYYKKT+NGRLPVKWMMAPEALFDR+YTHQSDVWSFG+L
 Sbjct: 409 LVTEDNVMKIAFDGLARGVHHIDYYKTSNGRLPVKWMMAPEALFDRVYTHQSDVWSFGIL 468
 Query: 601 LWEIFTLGGSPYPGVPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQ 660
 LWEIFTLGGSPYPG+PVEELP LL+EGRMD+P +C ELY +MR+CWAH PSQRPTFKQ
 Sbjct: 469 LWEIFTLGGSPYPG1PVEELFSLREGHMRMDRPPHCPPELYCLMRECWAAPSQRPTFKQ 528
 Query: 661 LVEVLDRIVALTSNQEYLDLSIPLDQYSPSFFDTRSSTCSSLGEDSVFSHEPLP 713
 LVE LD+++ L ++BYLDL + YSPS D SSTCSS DSVFSL+PLP
 Sbjct: 529 LVEALDKVL-LAVSEBYLDLRLTFGPYSPSGDA-SSTCSS-SDSVFSHDPLP 578

sp_vs P21802-15 Isoform 15 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 705 AA
 FGFR2_HUMAN (Human)] align

Score = 685 bits (1768), Expect = 0.0
 Identities = 390/758 (51%), Positives = 480/758 (63%), Gaps = 97/758 (12%)
 Query: 1 MWGWKCLLFWAVLVTATCTRAPTLPQDALPSSEDDDDDSSSEEKETDNTKPNPV 60
 M W + V+ ATL ARP+ +L E L E P
 Sbjct: 1 MVSWGRFICLVVVTMATLSLARPSFSLVEDTLEPEE-----PP 39
 Query: 61 APYWTSPEKMEKKLHAVPAAKTVFKCPSSGTPNPTLRLWKNGKEFKPDHR---IGGYKV 117
 Y S + +++ +++ +C + W K+G P++R IG Y
 Sbjct: 40 TKYQIS---QPEVYVAAPGSELEVRCLLKDA--VISWTKDGVHLGPNNRTVILGEY-- 91
 Query: 118 RYATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVE----- 158
 + + P D G Y C S + ++V +
 Sbjct: 92 -----LQIKGATPRDGLYACTASRTVDSETWYFMVNVTDAISSGDEDDTDGAEDFVS 145
 Query: 159 -----RSPHRPILQAGLPANKTVALGSNVEPMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
 R+P+ + V +V+F C +P P ++WLK NG + +
 Sbjct: 146 ENSNNKRAPYWTNTEKMEKRLHAVPAANTVKPRCPAGGNPMPTWRWLK---NGKEFKQE 201
 Query: 213 NL PYVQILKHSGINSSDAE-VLTLFNVTEAQSGEYVCKVSNVYICEANQSAWLTVT---- 266

+ + G + L + +V + G Y C V N G N + L V
 Sbjct: 202 H-----RIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSINHTYHLDVVERSPH 254
 Query: 267 RPVAKALEERPAVMTSPLYLEIIIICTGAFLISCMGLGSVIYYKMKSGTKSDFHQSMAVH 326
 RP+ +A PA ++ + ++ C + + I + K+G+K
 Sbjct: 255 RPILQA--GLPANASTVVGGDVEFVCK-VYSDAQPHIQWIKHVEKNGSKYGP----- 303
 Query: 327 KLAKSIPLRQQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMALAGVSEYELPEDPRWEI 384
 +P + + VSA+SS+SMNS LVR +RLSS+ TPMALAGVSEYELPEDP+WE
 Sbjct: 304 ---DGLPYLKVLKVSAESESSSMSNTPLVRITTRLSTATDPMLAGVSEYELPEDPKWEF 360
 Query: 385 PRDRLVLGKPLGECCFGQVVALEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEME 444
 PRD+L LGKPLGECCFGQVVA+AEA+G+DKDKP VAVKMLK DATEKDLSLDL+SEME
 Sbjct: 361 PRDKLTGKPLGECCFGQVVAEAVIDKDKPKAEVTAVKMLKDDATEKDLSLDLVSEME 420
 Query: 445 MMKMICGHKNI INNL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPPE 504
 MMKMICGHKNI INNL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEE
 Sbjct: 421 MMKMICGHKNI INNL ACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEE 480
 Query: 505 QLSKSDLVSCAYQVARGMEYLASKKC1IHRDLAARNVLVTEDNVMKIADFGLARDIHDY 564
 Q++ KDLVSC YQ+ARGMEYLAS+KC1IHRDLAARNVLVTE+NVMKIADFGLARDI++IDY
 Sbjct: 481 QMTPKDLVSCTYQLARGMEYLASQKCIHDLAARNVLVTEENNVMKIADFGLARDINNDY 540
 Query: 565 YKKTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLL 624
 YKKTNGRLPVKWMPEALFDRIY+YHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLL
 Sbjct: 541 YKKTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLMWEIFTLGGSPYPGPVVEELFKLL 600
 Query: 625 KEGRHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPL 684
 KEGRHRMDK+P+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL
 Sbjct: 601 KEGRHRMDK PANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEYLDLSQPL 660
 Query: 685 DQYSPSPFPDTRSSTCSSGEDSVFSHEPLPEEPCLP RHP 722
 +QYSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
 Sbjct: 661 EQYSPSPFPDTRS-CSSGDDSVFSDPMPYEPCLPQYP 697

tr Q59FL9 Fibroblast growth factor receptor 3 isoform 1 variant (Fragment) 879 AA
 Q59FL9_HUMAN [Homo sapiens (Human)] align

Score = 684 bits (1764), Expect = 0.0
 Identities = 346/539 (64%), Positives = 421/539 (78%), Gaps = 15/539 (2%)
 Query: 34 PSSEDDDDDDDSSEEKEDNTKPNPVAPYWTSPSPEKMEKKLHAVPAAKTVFKFCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPAAT TV+F+CP++G P
 Sbjct: 216 PSSGDEDGED-----EAEDTGVDTGAPYWRPERMDKLLAVPAANTVFRCPAAGNP 269
 Query: 94 NPTRLWLKNKGKEFKPDKDHRRIGGYKVRATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 270 TPSISWLKNGREFRGEHRIGGIKLHRQQWSLVMESVVPSDRGNYTCVVENKFEGSIRQTYT 329
 Query: 154 LDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK+GPDN 213
 LDV+ERSPhRPILQAGLPAN+T LGS+VEF CKVYSD OPHIQWLKH+EVNGSK+GPD
 Sbjct: 330 LDVLERSPhRPILQAGLPANQTAVLGSDEVFHCKVYSDAQPHIQWLKHIEVNGSKVGPDG 389
 Query: 214 LPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNVYIGEANQSAWLTVTRPVAK 271
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +
 Sbjct: 390 TPYVTVLKTAGANTTDEKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHSAWLVVL-PAEE 448
 Query: 272 ALEERPAVMTSPLYLEIIIICTGAFLISCMGLGSVIYYKMKSGTKSDFHQSMAVHKLAKS 331
 L E A +Y I+ Y G FL ++ +V + ++S KK VHK+++
 Sbjct: 449 ELVE--ADEAGSVYAGILSYVGFFFLFILVVAATLCRLRSPPKKG--LGSPVHKISR- 503
 Query: 332 IPRLRQQVTVSADSSASMNSGVLLVRPSRLSSGTPMLAGVSEYELPEDPRWEIPLRDLV 391
 PL+RQ VS +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L
 Sbjct: 504 FPLKRQ-QVSLESNASMSSNTFLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 562
 Query: 392 GKPLGEGCFGQVVALEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLDLISEMEMMMKIGK 451
 GKPLGEGCFGQVVA+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMMKIGK
 Sbjct: 563 GKPLGEGCFGQVVALEAIGLDKDKRAAKPVTVAVKMLKDDATKDLSLDLVSEMEMMMKIGK 622
 Query: 452 HKNIINNLACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPPEQQLSSKDL 511
 HKNIINNL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL
 Sbjct: 623 HKNIINNLACTQGGPLYVLVVEYAAKGNLREFLARRPPGLDYSFDTCKPPEEQLTFKDL 682
 Query: 512 VSCAYQVARGMEYLASKKC1IHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKTTN 570
 VSCAYQVARGMEYLAS+KC1IHRDLAARNVLVTEDNVMKIADFGLARD+H++DYYKTTN
 Sbjct: 683 VSCAYQVARGMEYLASQKCIHDLAARNVLVTEDNVMKIADFGLARDVHNLDYYKTTN 741

tr A8E633 Putative uncharacterized protein (Fragment) [Homo sapiens (Human)] 480 AA
 A8E633_HUMAN align

Score = 646 bits (1667), Expect = 0.0
 Identities = 328/474 (69%), Positives = 383/474 (80%), Gaps = 9/474 (1%)

Query: 243 SGEYVCKVSNYIGEANQSAWLTTRPVAKALEERPAVMTSPLYLEIIIICTGAFLISCM 302
 +GEY C N IG ++ SAWL V P + L E A +Y I+ Y G FL ++
 Sbjct: 8 AGEYTCAGNSIGFSHHSALVVL-PAEEELVE--ADEAGSVYAGILSYGVGFFLFILVV 64

Query: 303 GSIIYKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSS 362
 +V + +++S KK VH++ PL+RQV S +S+ASM+S LVR +RLSS
 Sbjct: 65 AAVTLCRLSRSPKKKG--LGSPTVHKISR-FPLKRQV--SLESNASMSSNTPLVRIARLSS 119

Query: 363 SGTPMLAGVSEYELPEDPRWELPRDRVLGKPLGEGCPGQVVAEEAIGLDKDKPNRVTKV 422
 P LA VSE ELP DP+WEI R RL LGKPLGEGCPGQVVAEEAIG+DKD+ + V
 Sbjct: 120 GEGPTLANVSELELPADPKWELSRAARLTLGKPLGEGCPGQVVAEEAIGIDKDRAAKPVT 179

Query: 423 AVKMLKSDATEKDLSDLISEMEMMMKMGKHKNIIINLLACTQDGPLYVIVEYASKGNLRE 482
 AVKMLK DAT+KDLSDL+SEMEMMMKMGKHKNIIINLL ACTQ GPLYV+VEYA+KGNLRE
 Sbjct: 180 AVKMLKDDATDKDLSDLVSEMEMMMKMGKHKNIIINLLACTQGGPLYVLVEYAAGKNLRE 239

Query: 483 YLQARRPPGLECYCYNPSHNPPEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLAARNVLW 542
 +L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLASKKCIIHRDLAARNVLW
 Sbjct: 240 FLRARRPPGLDYSFDTCKPPEQLTFKDLVSCAYQVARGMEYLASKKCIIHRDLAARNVLW 299

Query: 543 TEDNVMKIADEFGGLARDIHHIDYYKKTTNGRLPVKWMAPPEALFDRIYTHQSDVWSFGVLLW 602
 TEDNVMKIADEFGGLARD+H++DYKKTTNGRLPVKWMAPPEALFDRIYTHQSDVWSFGVLLW
 Sbjct: 300 TEDNVMKIADEFGGLARDVHNLDYKKTTNGRLPVKWMAPPEALFDRIYTHQSDVWSFGVLLW 359

Query: 603 EIFTLGGSPYGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLV 662
 EIFTLGGSPYGP+PVEELFKLLKEGHRMDK+PCT++LYM+MR+CWHA PSQRPTFKQLV
 Sbjct: 360 EIFTLGGSPYGPVVEELFKLLKEGHRMDKPNCTHDLYMIMRECWAAPSQRPTFKQLV 419

Query: 663 EVLDRIVALTSNQEYLDLSIPLDQYSQSFDPDSTSCTSSGEDSVFSHEPLPEEP 716
 E LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 420 EDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS-SSGDDSVFAHDLLPPAP 472

tr Q0IJ44 FGFR3 protein (Fragment) [FGFR3] [Homo sapiens (Human)] 480 AA
 Q0IJ44_HUMAN align

Score = 646 bits (1666), Expect = 0.0
 Identities = 328/474 (69%), Positives = 383/474 (80%), Gaps = 9/474 (1%)

Query: 243 SGEYVCKVSNYIGEANQSAWLTTRPVAKALEERPAVMTSPLYLEIIIICTGAFLISCM 302
 +GEY C N IG ++ SAWL V P + L E A +Y I+ Y G FL ++
 Sbjct: 8 AGEYTCAGNSIGFSHHSALVVL-PAEEELVE--ADEAGSVYAGILSYGVGFFLFILVV 64

Query: 303 GSIIYKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSS 362
 +V + +++S KK VH++ PL+RQV S +S+ASM+S LVR +RLSS
 Sbjct: 65 AAVTLCRLSRSPKKKG--LGSPTVHKISR-FPLKRQV--SLESNASMSSNTPLVRIARLSS 119

Query: 363 SGTPMLAGVSEYELPEDPRWELPRDRVLGKPLGEGCPGQVVAEEAIGLDKDKPNRVTKV 422
 P LA VSE ELP DP+WEI R RL LGKPLGEGCPGQVVAEEAIG+DKD+ + V
 Sbjct: 120 GEGPTLANVSELELPADPKWELSRAARLTLGKPLGEGCPGQVVAEEAIGIDKDRAAKPVT 179

Query: 423 AVKMLKSDATEKDLSDLISEMEMMMKMGKHKNIIINLLACTQDGPLYVIVEYASKGNLRE 482
 AVKMLK DAT+KDLSDL+SEMEMMMKMGKHKNIIINLL ACTQ GPLYV+VEYA+KGNLRE
 Sbjct: 180 AVKMLKDDATDKDLSDLVSEMEMMMKMGKHKNIIINLLACTQGGPLYVLVEYAAGKNLRE 239

Query: 483 YLQARRPPGLECYCYNPSHNPPEQLSSKDLVSCAYQVARGMEYLASKKCIIHRDLAARNVLW 542
 +L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLASKKCIIHRDLAARNVLW
 Sbjct: 240 FLRARRPPGLDYSFDTCKPPEQLTFKDLVSCAYQVARGMEYLASKKCIIHRDLAARNVLW 299

Query: 543 TEDNVMKIADEFGGLARDIHHIDYYKKTTNGRLPVKWMAPPEALFDRIYTHQSDVWSFGVLLW 602
 TEDNVMKIADEFGGLARD+H++DYKKTTNGRLPVKWMAPPEALFDRIYTHQSDVWSFGVLLW
 Sbjct: 300 TEDNVMKIADEFGGLARDVHNLDYKKTTNGRLPVKWMAPPEALFDRIYTHQSDVWSFGVLLW 359

Query: 603 EIFTLGGSPYGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLV 662
 EIFTLGGSPYGP+PVEELFKLLKEGHRMDK+PCT++LYM+MR+CWHA PSQRPTFKQLV
 Sbjct: 360 EIFTLGGSPYGPVVEELFKLLKEGHRMDKPNCTHDLYMIMRECWAAPSQRPTFKQLV 419

Query: 663 EVLDRIVALTSNQEYLDLSIPLDQYSQSFDPDSTSCTSSGEDSVFSHEPLPEEP 716
 E LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 420 EDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS-SSGDDSVFAHDLLPPAP 472

sp_vs P22607-3 Isoform 3 of P22607 - Homo sapiens (Human) [FGFR3] [Homo sapiens] 694 AA
 FGFR3_HUMAN (Human) align

Score = 625 bits (1611), Expect = e-178
 Identities = 332/547 (60%), Positives = 393/547 (71%), Gaps = 32/547 (5%)

Query: 176 VALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPVQIWKHSGINSSDAEVTLT 235
 V + V F C + P P I WLK NG + ++ L+H + L +
 Sbjct: 166 VPAANTVRFRCPAAGNPTPSISWLK---NGREFRGEHRIGGIKLRHQWS----LVM 215

Query: 236 FNVTEAQSGEYVKVSNYIGEANQS AWT-----RVAKALEERPAVMTSPLYLEIII 290
 V + G Y C V N G Q+ L V RP+ +A PA T+ L ++
 Sbjct: 216 ESVVPDSDRGNYTCVVENKFGSI RQTYTLDVLERSPHRPILQA--GLPANQTAVLGSDV 273

Query: 291 YCTGAFLISCMLGSVIYKMKSGTKSDFHQSMAVHKLA KS-IPLRRQVTVSADSSASMN 349
 +C +Y + H ++ K+ P + VS +S+ASM+
 Sbjct: 274 HCK-----VYSDAQPHIQWLKHVEVNGSKVGPDT PYVTVLKVSLESNASMS 320

Query: 350 SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI 409
 S LVR -RLSS P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVVAEAI 380

Query: 410 GLDKDKPNRVTKVAVKMLKSDATEKDLSLDSLISEMEMMMK MIGKHKNI INLL ACTQ GPLY 469
 G+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMMK MIGKHKNI INLL ACTQ GPLY 400

Query: 470 VIVEASKGNLREYLQARRPPGLEYCNPSHNPEEQLSSKDLVSCAYQVARGMEYLASK 529
 V+VBYA+KGNLRE+L+ARRPGL +Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+K
 Sbjct: 441 VLVEYAAKGNLREFLRARPPGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQK 500

Query: 530 CIHRDLAARNVLVLTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAP EALFDRIYT 589
 CIHRDLAARNVLVLTEDNVMKIADFGLARD+H+DYYKKTTNGRLPVKWMAP EALFDRIYT 560

Query: 590 HQSDVWSFGVLLWEITLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWH 649
 HQSDVWSFGVLLWEITLGGSPYPGP+VVEELFKLLKEGHRMDKP+NCT++LYM+MR+CWH
 Sbjct: 561 HQSDVWSFGVLLWEITLGGSPYPGP+VVEELFKLLKEGHRMDKPANCTHDLYMIMRECWH 620

Query: 650 AVPSQRPTFKOLVEVLDRLIVALTSNQEYLDLSIPLDQYSPSPFPDRSSTCSSGEDSVFSH 709
 A PSQRPTFKOLVE LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H
 Sbjct: 621 AAPSRQRTFKOLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS-SSGDDSVFAH 679

Query: 710 EPLPEEP 716
 + LP P
 Sbjct: 680 DLLPPAP 686

Score = 280 bits (717), Expect = 5e-75
 Identities = 131/213 (61%), Positives = 165/213 (77%), Gaps = 7/213 (3%)

Query: 34 PSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPSPEKMEKKLHAVPAAKTVKFKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPAA TV+F+CP++G P
 Sbjct: 129 PSSEDDDEDGED-----EAEDTGVDTGAPYWT RPERMDKKL LAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+S+VVPSD+GNYTC+VEN+ +GSI TY
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQOWSLVMEVSVPSDRGNYTCVVENKFGSI RQTYT 242

Query: 154 LDVVERSPHRPILQAGL PANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
 LDV+ERSPHRPILQAGL PAN+T LGS+VEF CKVYSD QPHIQWLKH-EVNGSK+GPD
 Sbjct: 243 LDVLERSPHRPILQAGL PANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDG 302

Query: 214 LPYVQILKHS-GINSSDAEVTLFNVTTEAQSGE 245
 PYV +LK S N+S + L + SGE
 Sbjct: 303 TPYVITVLKVSLESNASMSSNTPLVRIARLSSCE 335

```
tr Q59F30      Fibroblast growth factor receptor 4 variant (Fragment) [Homo sapiens 1034 AA
Q59F30_HUMAN   (Human)] align
```

Score = 553 bits (1426), Expect = e-157
 Identities = 285/450 (63%), Positives = 348/450 (77%), Gaps = 13/450 (2%)

Query: 268 PVAKALEERPAVMTSP--LYLEIIIYCTGAFLISCMLGSVIYKMKSGTKKSDFHSQ--M 323
 P A+A E+ +P Y +II+Y +G+ ++ +L ++ ++ G H +
 Sbjct: 580 PCARAEEDPTWTAAPEARYTDIILYASGSLALAVL--LLARLYRGQALHGRHPRPPA 636

Query: 324 AVHKLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWE 383
 V KL++ PL RQ ++ +SS +S LVR RLSSSG +LAG+ +LP DP WE
 Sbjct: 637 TVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRLSSSGPALLAGLVSDLPLDPLWE 693

Query: 384 LPRDRLVLGKPLGEGCFGQVVAEAGLKD KPNRVTKVAVKMLKSDATEKDLSLDSLISEM 443
 PRDRLVLGKPLGEGCFGQVVAEAG+D +P++ + VAVKMLK +A++KDL+DL+SEM
 Sbjct: 694 FPRDRLVLGKPLGEGCFGQVVAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEM 753

Query: 444 EMMMKIGKHKNI INLL ACTQGDGPLYVIVEASKGNLREYLQARRPPGLEYCYNPSHNPE 503
 E+MK+IG+HKNI INLL CTQ+GPLYVIVE A+KGNLRE+L+ARRPPG + + + E

```

Sbjct: 754 EVMKLIGRHKNIIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLS PDGPRSSE 813
Query: 504 EQLSSKDLVSCAYQVARGMEYLASKKCIHRLAARNVLVTEEDNVMKIADFGGLARDIHID 563
      LS LVSCAYQVARGM+YL S+KCIHRLAARNVLVTEEDNVMKIADFGGLAR +HHID
Sbjct: 814 GPLSFVPLVSCAYQVARGMQYLESRKCIHRLAARNVLVTEEDNVMKIADFGGLARGVHHID 873
Query: 564 YYKKTTNGRLPVKWMMAPEALFDRIYTHQSDVWSFGVLLWEITLGGSPYPGPVVEELFKL 623
      YYKKT+NGRLPVKWMMAPEALFDR+YTHQSDVWSFG+LLWEITLGGSPYPG+PVEELF L
Sbjct: 874 YYKKTSNGLPVLVSCAYQVARGMQYLESRKCIHRLAARNVLVTEEDNVMKIADFGGLARGVHHID 933
Query: 624 LKEGHHRMDKPSNCTNELYMMRDCWHAVPSPQRPTFKQLVEVLDRAVALTSNQEYLDLSIP 683
      L+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD+++ L ++EYLDL +
Sbjct: 934 LREGHHRMDRPPHCPELYGLMRECWHAPSQRPTFKQLVEALDKVL-LAVSEEYLDLRLT 992
Query: 684 LDQYSPSPFPDTRSSTCSSGEDSVFSHEPLP 713
      YSPS D SSTCSS DSVFSH+PLP
Sbjct: 993 FGPYSPSPGGDA-SSTCSS-SDSVFSHDPLP 1020

```

Score = 295 bits (754). Expect = 2e-79
 Identities = 134/209 (64%), Positives = 164/209 (78%)

```

Query: 57 PNPVAPYWTSPKMEKKLHAVPAAKTVFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYK 116
      P P APYWT P++MEKKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG +
Sbjct: 257 PCPPAPYWTQPMERMEKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDQAFHGENRIGGIR 316
Query: 117 VRYATWSIIMDSVVPDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTV 176
      +R+ WS++M+S+VVP+D+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T
Sbjct: 317 LRHQHWSLVMESVVPSDRGTYTCLVENAVGSIRYNYLLDVLERSPHRPILQAGLPANTTA 376
Query: 177 ALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGGINSSDAEVLTLF 236
      +GS+VE +CKVYSD QPHIQWLKI +NGS G D PYVQ+LK + INSS+ EVL L
Sbjct: 377 VVGSDVELLCKVYSDAQPHIQWLKHIVINGSSGADGFPPYVQVLKTADINSSEEVLYLR 436
Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLT 265
      NV+ +GEY C N IG + QSAWLT
Sbjct: 437 NVSAEDAGEYTCLAGNSIGLSYQSAWLT 465

```

Subset of the database(s) listed below
 Number of letters searched: 35,064,127
 Number of sequences searched: 82,088

Database: UniProtKB_Homo sapiens
 Posted date: Nov 12, 2007 6:33 PM
 Number of letters in database: 25,263,043
 Number of sequences in database: 64,426

Database: UniProtKB_HUMAN.01
 Posted date: Nov 12, 2007 6:36 PM
 Number of letters in database: 9,801,084
 Number of sequences in database: 17,662

Lambda K H
 0.316 0.133 0.405

Gapped Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 59,077,092
 Number of Sequences: 2526181
 Number of extensions: 2919052
 Number of successful extensions: 266662
 Number of sequences better than 10.0: 1000
 Number of HSP's better than 10.0 without gapping: 1277
 Number of HSP's successfully gapped in prelim test: 935
 Number of HSP's that attempted gapping in prelim test: 15141
 Number of HSP's gapped (non-prelim): 6214
 length of query: 733
 length of database: 35,064,127
 effective HSP length: 114
 effective length of query: 619
 effective length of database: 25,706,095
 effective search space: 15912072805
 effective search space used: 15912072805
 T: 11
 A: 40
 X1: 16 (7.3 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (21.6 bits)
 S2: 68 (30.8 bits)
 Wallclock time: 4 seconds



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